OM protein - protein search, using sw model

July 22, 2003, 08:05:44; Search time 1.09218 Seconds (without alignments) 1830.070 Million cell updates/sec Run on:

US-09-806-703A-12 74 1 OYIKANSKFIGITEL 15

Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983\_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984\_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985\_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986\_DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988\_DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988\_DAT: geneseqp-embl/AA2000.DAT /geneseqp-embl/AA1998 /genesegp-embl/AA1989 geneseqp-emp1/AA1990 /SIDS2/gcddata/geneseq/geneseqp-embl/AA1991 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993 /geneseqp-embl/AA1993 /депеведр-ещр] 'SIDS2/gcgdata/geneseg, /gcgdata/geneseg/ gcgdata/geneseg/ SIDS2/g /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|    | Description              | Tetanis toxin enit | Universal T-cell e | Tetanna roxoid univ | Tetanus toxin frac | Iniversal helper | T-Welner enitone f | T-cell enitone nen | Tetanis toxoid eni | Tetanis Do enitone | Tetanus toxoid T c |
|----|--------------------------|--------------------|--------------------|---------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|    | ID                       | AAR06310           | AAW35506           | AAW11505            | AAW67033           | AAW71321         | AAY04051           | AAW67578           | AAW73220           | AAB45511           | AAY82637           |
|    | Query<br>Match Length DB | 15 11              | 15 18              | 15 18               | 15 19              | 15 19            | 15 20              | 15 20              | 15 20              | 15 21              | 15 21              |
| مو | Query<br>Match L         | 100.0              | 100.0              | 100.0               | 100.0              | 100.0            | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              |
|    | Score                    | 74                 | 74                 | 74                  | 74                 | 74               | 74                 | 74                 | 74                 | 74                 | 74                 |
|    | Result<br>No.            | -                  | 6                  | m                   | 4                  | S                | 9                  | 7                  | <b>6</b> 0         | σ                  | 10                 |

| н ехен  | Amino acid sequenc<br>Wild-type TTB30 (t<br>Tetanus Toxoid uni<br>Tetanus toxin T-ce<br>HER-2 B cell pepti<br>Tetanus toxoid TTB<br>Tetanus toxoid TT<br>Tetanus toxin P2 (<br>T-cell stimulatory<br>Clostridium tetani<br>Clostridium tetani<br>Tetanus toxoid pre |                                       | Amino acid residue Amino acid sequenc Amino acid sequenc Antigenic fragment Antigenic fragment Peptide 5 for pept HIV-derived lipope Peptide TT functio |
|---|---|---------------------------------------|---|
|   | 2333083355555555555555555555555555555555  | 22222222                              | 22 AAG62904<br>22 AAB31029<br>22 AAB31029<br>22 AAB31118<br>22 AAB1589<br>20 AAY26607<br>23 ABB09794  |
| 44 1000.0<br>44 1000.0<br>1000.0<br>1000.0<br>1000.0  | 000000000000000000000000000000000000000   | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 1000.0<br>1000.0<br>1000.0<br>1000.0<br>1000.0  |
| 11 12 12 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16 | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2   |                                       | ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩   |

## ALIGNMENTS

AAR06310 standard; protein; 15 AA. 04-DEC-1990 (first entry) AAR06310; AAR06310 ID AARC 

Tetanus toxin; vaccine; major histocompatibility complex; MHC; antimalarial.

Tetanus toxin epitope.

EP378881-A. Synthetic,

89EP-0203318 27-DEC-1989; 25-JUL-1990

89IT-0022409 89IT-0019110 16-NOV-1989; 17-JAN-1989; (ENIE ) ENIRICERCHE SPA.

Corradin G; Verdini AS, Bianchi E, Pessi A,

WPI; 1990-225582/30

Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used as universal carriers for prepn. of immunogenic conjugate(s) for use as vaccines.

us-09-806-703a-12.rag

1

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Epitopic peptides may be used with synthetic hapten derived from a pathogen to generate an immune response to the pathogen. Peptides are recognised by numerous T-helper call clones within the context of a wide range of alleles of the human MHC. The peptides may be used in an antimalarial vaccine inducing Ab.
                                                                                                  Length 15;
                                                                                                                Indels
                                                                                               Score 74; DB 11;
Pred. No. 3.9e-07;
Mismatches 0;
                                                                                                                                                                                        Ä
       Claim 1; Page 17; 20pp; English.
                                                                                                               ,
0
                                                                                                                                                                                    AAW35506 standard; peptide; 15
                                                                                               100.0%;
                                                                                                                              1 OYIKANSKFIGITEL 15
                                                                                                                                        1 OYIKANSKFIGITEL 15
                                                                response to P.falciparium.
                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                               15 AA;
                                                                               Sequence
                                                                                                                                                                                                     AAW35506;
                                                                                                                                                                             ò
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Gaps

. 0

T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.

Universal T-cell epitope peptide SEQ ID NO:8

(first entry)

22-APR-1998

Unidentified

WO9738011-A1

16-OCT-1997

97WO-DE00146.

96DK-0000398. 03-APR-1996;

(PEPR-) PEPRESEARCH AS

Heegaard PMH, Jakobsen PH;

WPI; 1997-512645/47.

Non-dendritic peptide carrier linked to a solid phase - usefu diagnostic agent and as a scaffold for production of chemical derivatives

Example 20; Page 124; 262pp; English:

A non-dendritic peptide carrier (A) has been developed which is coupled through a linker to a solid phase, forming a complex of (A) solid phase.

Where (A) comprises 10-50; amino acids capable of forming a secondary structure in a benign buffer after liberation from the solid phase, and further the (A) solid phase complex comprises an immunogenic substance represents a peptide used in an example from the present sequence (A) solid phase complex can be used as a scaffold for the production of the present invention. An constant of the present invention and inmunostimulating Complex (Iscom) resulting an an immunostimulating Complex (Iscom) resulting an for the promotion of cell-attachment to solution by conjugation. (A) derivatised with mg fibronectin-, laminin- or vitronectin-like for the chemical coupling of antigenic Also a derivatised (A) can be used is used

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   for the selection of specifically-binding aptamers or as a diagnostic agent. Such diagnostic-(A) molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an
                                                                                            Gaps
                                                                                                                                                                                                                                                      numanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;
fusion protein; chimera; tetanus toxoid; helper T cell epitope;
antigen presentation; ds.
                                                                                           ö
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Somasundaram C;
                                                                                          ö
                                                                    100.0%; Score 74; DB 18; 100.0%; Pred. No. 3.9e-07;
                             infectious, autoimmune or cancerous disease.
                                                                                         0; Mismatches
                                                                                                                                                                                                                                           Tetanus toxoid universal Th epitope TT830.
for the selection of specifically-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                Graziano R,
                                                                                                                                                                                AAW11505 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                    96WO-US09988.
                                                                                                            1 OYIKANSKFIGITEL 15
                                                                                                                            OYIKANSKFIGITEL 15
                                                                                                                                                                                                                        (first entry)
                                                                              Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Deo YM, Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-052242/05.
N-PSDB; AAT58127.
                                                                                                                                                                                                                                                                                                                                                                                                          (MEDA-) MEDAREX INC
                                                  15 AA;
                                                                                                                                                                                                                                                                                                                          WO9640789-A1
                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                         24-SEP-1997
                                                                                                                                                                                                                                                                                                                                              19-DEC-1996
                                                  Sequence
                                                                     Query Match
                                                                                                                                                                                                     AAW11505;
                                                                                                                                                             RESULT 3
                                                                                                                                                                       AAW11505
8X33333
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encoding heavy chain sequences from the humanised anti-Pc gamma RI monoclonal antibody H22. The resulting fusion protein was shown to be significantly more efficient in antigen presentation and T cell stimulation that the TH30 epitope alone. A similar fusion construct was prepared coding for a mutant, antagonistic form of the epitope (designated TT8313S) fused to the anti-Pc gamma RI. The Fab22-TT831S is at least 100 times more effective than TT833S in inhibiting T cell activation. Synthetic DNA coding for the wild-type universal Th epitope from tetanus toxoid, designated TT830, was fused to the 3'-end of DNA 100.0%; Score 74; DB 18; Length 15; 100.0%; Pred. No. 3.9e-07; ive 0; Mismatches 0; Indels Local Similarity nes 15; Conserv 15 AA; Sequence Query Match

Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection

Example 7; Fig 24; 115pp; English.

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Conservative

Matches

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Gaps

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26-NOV-1998

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carponydrate peptide conjugate used as vaccine - comprises carrier with dendrimeric poly-lysine enabling multiple epitopes to be covalently attached
                                                                                                                                               Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate; dendrimeric poly-lysine; epitope; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lo-man R;
                                                                                                                Tetanus toxin fragment (residues 830-844).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 13; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leclerc C,
AAW67033 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                         98WO-EP01922
                                                                                                                                                                                                                                                                                                                                                                               97US-0041726
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cantacuzene D,
                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-557071/47.
                                                                                                                                                                                                                     Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                           27-MAR-1998;
                                                                                                                                                                                                                                                               WO9843677-A1
                                                                              15-DEC-1998
                                                                                                                                                                                                                                                                                                    08-OCT-1998
                                           AAW67033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bay S,
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The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple comprises a carrier with a dendrimeric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an entibody purified from biological fluid or cells of organisms antibody multiple carbohydrate peptide conjugate, and (2) a diagnosis of the carbohydrate peptide conjugate, and (2) a diagnosis kit are used to provide pharmaceutical compositions and capanisms kit are used to provide pharmaceutical compositions and capanisms kit are used to provide pharmaceutical compositions and capanisms viral infections caused by hepatitis virus, HIV or cytomegalo against viral infections caused by hepatitis virus, HIV or cytomegalo virus. They can be used to enhance immune responses, of humans and animals against bacterial infections. The call responses, of humans and animals against bacterial infections. The carbohydrate peptide conjugate stimulates the antibody and T-cell capanism without stimulating undesired immune responses. The composition is capanish the increasing the survival of tumour bearing humans and mineral capanisms. animals. The present sequence corresponds to residues 830-844 of tetanus toxin. The synthetic peptide corresponding to this sequence may be used as an epitope in a carbohydrate peptide conjugate.

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Gaps
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                                                                                                                                            Length 15;
                                                                                                                                                 0; Indels
                                                                                                                                            100.0%; Score 74; DB 19; 100.0%; Pred. No. 3.9e-07;
                                                                                                                                                 Mismatches
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                                                                                                                                                       1 QYIKANSKFIGITEL 15
                                                                                                                                                  15; Conservative
                                                                                                                                               Local Similarity
                                                                                                                                        15 AA;
                                                                                                                                        Sequence
                                                                                                                                            Query Match
                                                                                                                                                   Matches
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AAW71321 standard; peptide; 15 AA.
OYIKANSKFIGITEL 15
                                   RESULT 5
AAW71321
ID AAW71
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AAW71321;

Clostridium tetani

WO9948925-A1

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AW71321-22 represent universal helper T-cell epitopes derived from tetanus toxin. They are used to enhance host immune response to vaccines. The specification describes a Plasmodium yoelil liver stage protein designated PyHSP1. This 17 kDa hepatic and erythrocytic stage protein designated PyHSP1. This protein elicits a response (From an Ig1 monoclonal antibody designated Navy Yoelii Liver Stage) (NYLS3). This antibody does not recognise sporozoites, but does recognise P. yoelii liver stage parasites. NYLS3 eliminates upto 90% of liver stage parasites. The specification describes a vaccine for reducing the severity or incidence of infection by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises exon 1 and part of exon 2 of the PyHEP17 gene.
                                                                                                                                                                                                                                                                                                                                                                                                               vaccine for protecting mammal against infection by malaria caused by Plasmodium species - comprises a first nucleic acid encoding a first polypeptide capable of eliciting an immune reaction against an antigen expressed during the liver
                                                  Liver stage, Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3; hepatic and erythrocytic stage protein; PyHEP17; vaccine; malaria parasite; teanus toxin; P2; helper T-cell epitope.
                  Universal helper T-cell epitope P2 derived from tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                       Hoffman SL;
                                                                                                                                                                                                                                                                                                                                                       Hedstrom RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 12; 24pp; English.
                                                                                                                                                                                                                                                                                        94US-0319704.
                                                                                                                                                                                                                                                      94US-0319704.
                                                                                                                                                                                                                                                                                                                                                         Doolan DĹ,
                                                                                                                                                                                                                                                                                                                          (USNA ) US SEC OF NAVY
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-541794/46.
                                                                                                                                                    Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                                                                                                                                                                                             Charoenvit Y,
                                                                                                                                                                                                                                                                                          07-OCT-1994;
                                                                                                                                                                                                                                                           07-0CT-1994;
                                                                                                                                                                                      US5814617-A
                                                                                                                                                                                                                         29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                  Synthetic
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Gaps . 0 Length 15; Indels ö 100.0%; Score 74; DB 19; 100.0%; Pred. No. 3.9e-07; :ive 0; Mismatches 0; 1 QYIKANSKFIGITEL 15 QYIKANSKFIGITEL 15 15; Conservative Query Match Best Local Similarity Matches

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Covalently reactive antigen analog; CRAA; catalytic antibody; electrophilic reaction centre; phosphonate; boronate; vaccine; transition state analog; TSA; isostere; gpl20; HIV-1; T-helper; tetanus; toxoid; B-T-epitope.
                                                                                                                                                  T-Helper epitope from tetanus toxoid.
                                                                             AAY04051 standard; peptide; 15 AA.
                                                                                                                             04-JAN-2000 (first entry)
                                                                                                       AAY04051;
                                                          RESULT 6
                                                                     AAY0405
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comprising

Total number of

DB DB

Minimum Maximum Database :

Perfect score:

Run on:

Sequence:

Scoring table:

toxoid

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PSMpep010 - P30 in
PSMpep011 - P30 in
PSMpep012 - P30 in
LHRH-containing im
                                                Tetanus Toxoid uni
Tetanus toxin T-ce
HER-2 B cell pepti
Tetanus toxoid TT9
                                                                                                                                                                                                              Tetanus toxoid 830
Amyloid beta/tetan
Tetanus toxoid epi
          CD4+ T cell epitop
Clostridium tetani
                              Amino acid sequenc
Universal tetanus
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Immunogenic branch
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                                                                                                                                                                                                                                                                                                peptide which ma
                                                                                          Tetanus toxoid
                                                                                                    Tetanus toxoi
Tetanus toxoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic peptide(s) used as universal carrier's - for preparing
                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                 retanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria vaccine; major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..14
/label= active fragment (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic conjugate constituent peptide, TT3
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                           AAB49090
AAU11429
                                                                                                           AAB46176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR11896 standard, peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corradin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90EP-0202948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89IT-0022355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1991 (first entry)
(ENIE ) ENIRICERCHE SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pessi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-141874/20
                                                                                                                               001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP427347-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bianchi E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR11896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                     AAR11896
T-cell epitope pep
Tetanus toxoid epi
Tetanus P30 epitop
Tetanus toxin T ce
Foreign epitope P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic conjug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broad range helper
Tetanus toxin frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetanus toxoid pro
T-cell antigen TT3
                                                              July 22, 2003, 08:05:44; Search time 1.52905 Seconds (without alignments) 1830.070 Million cell updates/sec
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                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
                                                                                                                                                                                                  908470
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                112
1 FNNFTVSFWLRVPKVSASHLE 21
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AAW67034
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AAW73222
AAB45512
AAY99876
AAY92626
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AAR88397
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                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                        US-09-806-703A-14
                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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113
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Match Length
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1000.00

112

Score

Result Š.

#### Tue Jul 22 12:43:19 2003

### us-09-806-703a-14.rag

RESILT 4 AAW46449 ID

AAW46449;

AAW46449 standard; Peptide; 21 AA.

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100.0%; Score 112;
                                                                                                                                                                                                                        Ouery Match
           immunogenic conjugates used as vaccines against Plasmodium
                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                              100.0%; Pred. No.
           falciparum
                                                                                                                                                                                                                                                                                              0: Mismatch
XX
PS
XX
CC
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                             21; Conservative
          Claim 1; page 13; 16pp; English.
                                                                                                                                                                                                                                              1 FNNFTVSFWLRVPKVSASHLE 21 ||||||||||| 1 FNNFTVSFWLRVPKVSASHLE 21
          This peptide corresps. to residues 947-967 of Tetanus toxin. It can be used as a universal carrier for the prepn. of an immunogenic conjugate. It is covalently bound to a peptide or polysaccharide
                                                                                                                                                                                                                    Db
           hapten derived from a pathogen. This conjugate can be used as a vaccine for malaria. This peptide is recognised by different Thelper cell clones in association with alleles of the human MHC.
                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                    AAR88397
                                                                                                                                                                                                                              AAR88397 standard; Peptide; 21 AA.
           It contains 2 epitopes: (a) 953-967, recognised by DR5-restricted clones; and (b) 947-960, recognised by all other DR and DP-
                                                                                                                                                                                                                    ΙĎ
CC
           restricted clones.
                                                                                                                                                                                                                               AAR88397:
                                                                                                                                                                                                                    DT
                                                                                                                                                                                                                               12-JUN-1996 (first entry)
           Sequence 21 AA;
                                                                                                                                                                                                                    XX
                                                          100.0%; Score 112; DB 12; Length 21; 100.0%; Pred. No. 3.9e-12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                               T-cell antigen TT3 peptide.
    Query Match
                                                                                                                                                                                                                    XX
               Local Similarity
                                                                                                                                                                                                                              T-antigen; vaccine; antibody; T-cell; T-alpha-helix; coiled-coil heterodimer; cc
    Matches
                          21; Conservative
                                                                                                                                                  0; Gaps
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XX
                           1 FNNFTVSFWLRVPKVSASHLE 21
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                                                                                                                                                                                                                               Synthetic.
                           Db
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                                                                                                                                                                                                                               WO9531480-A1.
                                                                                                                                                                                                                               23-NOV-1995.
RESULT 2
AAW06130
                                                                                                                                                                                                                    XX
           AAW06130 standard; Peptide; 21 AA.
                                                                                                                                                                                                                               18-MAY-1995;
                                                                                                                                                                                                                                                                95WO-CA00293.
ID
                                                                                                                                                                                                                                                                94US-0245507.
AC
XX
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                                                                                                                                                                                                                               18-MAY-1994:
           AAW06130:
           07-FEB-1997 (first entry)
                                                                                                                                                                                                                    PA
                                                                                                                                                                                                                                (SPIS-) SPI SYNTHETIC PEPTIDES INC.
XX
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                                                                                                                                                                                                                               Cachia PJ, Hodges RS, Houston ME,
          Tetanus toxoid protein T-cell epitope.
XX
KW
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                                                                                                                                                                                                                               Zhou NE:
           Cholesteryl ester transfer protein; CETP; antigen; vaccine; cardiovascular disease; atherosclerosis; tetanus toxoid;
                                                                                                                                                                                                                    XX
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                                                                                                                                                                                                                               WPI; 1996-010880/01.
KW
XX
           T-cell epitope.
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                                                                                                                                                                                                                               Hetero:dimeric polypeptide immunogen in with different antigens on each sub:unit
           Clostridium tetani.
XX
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                                                                                                                                                                                                                    XX
           WO9634888-A1.
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                                                                                                                                                                                                                               Claim 7; Page 62; 95pp; English.
PD
           07-NOV-1996.
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XX
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                                                                                                                                                                                                                                contained in one of the 2 subunits of ar
           01-MAY-1996;
                                             96WO-US06147.
                                                                                                                                                                                                                               heterodimer. Each core peptide is compi
internal AA repeat sequences. This pept
XX
PR
           01-MAY-1995:
                                             95US-0432483.
                                                                                                                                                                                                                    CC
                                                                                                                                                                                                                               to the core peptide through covalent lir
internal repeats. The 2 subunits of the
in a stable alpha-helical coiled-coil co
           (TCEL-) T CELL SCI INC.
XX
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                                                                                                                                                                                                                               stoichiometry, and the peptide antigen is surfaces of the configuration. The hete
           Rittershaus CW, Thomas LJ;
ХX
DR
           WPI: 1996-506103/50.
                                                                                                                                                                                                                                synthetic vaccine (optionally multivaler
                                                                                                                                                                                                                    CC
                                                                                                                                                                                                                               antibodies.
           Cholesteryl ester transfer protein B cell epitope linked to T cell epitope - used to generate vaccine to regulate CETP activity for
                                                                                                                                                                                                                    ХX
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                     21 AA;
РТ
           decreasing the risk of developing a cardiovascular disease e.g.
                                                                                                                                                                                                                                                                              100.0%; Score 112;
100.0%; Pred. No.
           atherosclerosis
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                         Best Local Similarity 100.0%;
            Claim 11; Page 43; 72pp; English.
                                                                                                                                                                                                                                             21; Conservative
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              Thelper T-cell epitope (AAW06130) comprises amino acids 947-967
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SMART; SM00261; FU; SM0220; STKC; 1.
SMART; SM00219; TVRC; 1.
SMART; SM00219; TVRC; 1.
SMART; SM00219; TVRC; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE TYR; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
TYrosine-protein kinase; ATF-binding; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                   01-5AN-1990 (Rel. 13, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (BC 2.7.1.112)
                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Cyptinodontiformes, Poeciliidae, Xiphophorus.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MIRDLINES-20015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Telling A., Robertson S.M., Schartl M.;
Thovel putative receptor tyrosine kinase encoded by the melanoma-
inducing Tu locus in Xiphophorus.";
Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÚBCELLULÂR LÔCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                           1230 DODPPERGA--PPSTFKGTPT------AENPEYL
                                                                                                                                                                                                                             XMRK OR TU.
Xiphophorus maculatus (Southern platyfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X16891; CAA34770.2; ---
PRR; S06142; S06142.
PRSSP; P11362; 1FGK.
INTERPO; IPR000199; EGFR L domain.
INTERPO; IPR000199; EUK_DKIABS.
INTERPO; IPR002174; FUTIN-11ke.
INTERPO; IPR001245; TYT_DKIABSE.
PEam; PF00069; PKIABSE; I.
PEam; PF00069; PKIABSE; I.
PEAM; PF01030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOGS: PROMOIN EUK_DKIABSE; I.
SANDH. SMOOGS: PTREINASE.
                                                                                                                                           STANDARD;
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AC P13388;
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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MEDLINE=90311312; PubMed=2164210; Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Todarco G.J., Shoyab M.; Molecular cloning and expression of an additional epidermal growth factor receptor-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=9328282; PubMed=7685162;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                               SEQUENCE FROM N.A.
MEDLINE-gold3234; PubMed=2687875;
Kraus M.H., 18shig W., Miki T., Popescu N.C., Aaronson S.A.;
"Isolation and characterization of ERBB3, a third member of the RBB4 pelderaral growth factor receptor family: evidence for overexpression in a subset of human mammary tumors.";
proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                                                                                                                                                                                                                              tyrosine Kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP
                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                         SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
    1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFY 1011
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TGYLVIMMMPENMTSLSVFQNLEIIRGRTTFSRGFSFVVVQVRHLQWLGLRSLKEVSAGN 465
                                                 531
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                                                                            466 VILKNTLOLRYANTINWRRLFRSEDQSIEYDART-----ENQTCNNECSEDGCWGPGP
                                                                                                            TOCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCV
                                                                                                                                           TMCVSCLHVDRGGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCS
                                                                                                                                                                           592 ACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE
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+ protein

tyrosine phosphate.

(POTENTIAL)

NEUREGULINS AND NTAK

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IFR000719; Euk phinase.
R InterPro; IPR000719; Euk phinase.
R InterPro; IPR001745; Furin-like.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF001030; Purin-like; 1.
R Pfam; PF001030; Purin-like; 1.
R Pfam; PF001030; Prorp. 1.
R SMART; SM00261; FU; 3.
R SMART; SM00219; TyrKc; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; PALSE NEG.
R PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
R PROSITE; PS00101; PROTEIN KINASE TYR; FALSE_NEG.
R PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
R PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
R PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
R Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
SECRETED (SHORT FORM).

-1-ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
-1-TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
-1-DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH12 OR SH13 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-1-FTM: LIGAND-BINDING INTERASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF PROPERTY.
-1-DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
-1-SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR000494; EGFR L domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M29366; AAA35790.1; -. EMBL; M34309; AAA35979.1; -. EMBL; S61953; AAB26935.1; -.
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Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

01-MAY-1991 (Rel. 18, Created)
10-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbb-3 precursor (EC 2.7.1.112)
(c.erbb3) (Tyrosine kinase-type cell surface receptor HER3).

\$ 1342

STANDARD;

ERB3 HUMAN P21860;

HUMAN

| 301 CVTACPYNYLSTDVGSCTLVCPLHNQBVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 360 286 CVASCPHNFV-UDGTSCVRACPPDKMEND-KNGLKMCEPCGGLCPKACEGTGSGSRF0 341 361 AVTSANIQETGCKKIPGSLAFLPESFDGDPASNTAPLQPEQLOVFFTLEEITGYLXISA 420 342 TVDSSNIDGFANCTKILGNLDPLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLXIGS 401 421 WPDSLLPDLSVFONLQVIRGRILHNGAVS-LTLQGLGISWLGLRSLRELGSGLALIHNTH 479 102 WPDHMHNESVPSNLTTIGGRSLYNRGFSLLIMKNLNTSLGFRSLKEISAGRIYISANQ 461 403 WPDHMHNESVPSNLTTIGGRSLYNRGFSLLIMKNLNTTSLGFRSLKEISAGRIYISANQ 461 404 LCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCS 538 1  |   | 1011 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHRHRRSSTRSGGGDLTLGLE 1070  996 TNKKLEVETEEPELDLDLEAEED   |
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| \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8 \$ 8  | 6   | 8 4 8 4 8 4 8 8 8 8 8  |
| POTENTIAL.  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.  EXTRACELLULAR (POTENTIAL).  CYTOPLASHIC (POTENTIAL).  CYTOPLASHIC (POTENTIAL).  RY SIMILARITY.  BY SIMILARITY.   | 1 BY SIMILARITY.  9 BY SIMILARITY.  10 N-LINKED (GLCNAC ) (POTENTIAL).  11 N-LINKED (GLCNAC ) (POTENTIAL).  12 N-LINKED (GLCNAC ) (POTENTIAL).  13 N-LINKED (GLCNAC ) (POTENTIAL).  14 N-LINKED (GLCNAC ) (POTENTIAL).  15 N-LINKED (GLCNAC ) (POTENTIAL).  16 N-LINKED (GLCNAC ) (POTENTIAL).  17 N-LINKED (GLCNAC ) (POTENTIAL).  18 N-LINKED (GLCNAC ) (POTENTIAL).  19 N-LINKED (GLCNAC ) (POTENTIAL).  20 N-LINKED (GLCNAC ) (POTENTIAL).  31 SILSGGVYIEKNDKLCHMDTIDMEDIVEDERLITISASSK.  32 VEYTLAAV (IN SHORT ISOFORM).  33 SILSGGVYIEKNDKLCHMDTIDMEDIVEDERLITISASSK.  34 VEYTLAAV (IN SHORT ISOFORM).  36 N-S G (IN REF. 2).  37 SING SING SIN REF. 2).  41 E -> G (IN REF. 2).  41 REP. 20 (IN REF. 2). | 34.8%; Score 2382.5; DB 1; Length 1342;  Conservative 190; Mismatches 456; Indels 147; Gaps 35;  GLLLALLEPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYGGCQVVGGNLELTYLPT 67  GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYGTLYKLYERCEVVMGNLEIVLTGH 70  NASLSFLODIGEVQFNNFTVSFWLRVPKVSASHLEGRLRIYRGTQLFEDNYALA 121  |
| aplicing.<br>20 20 643<br>20 643<br>20 644<br>665 1342<br>715 742<br>717 742<br>718 742<br>719 764<br>710 208<br>710 208 | AA;<br>AA;<br>AA;<br>AA;<br>AA;<br>AB;<br>AB;<br>AB;<br>AB;<br>AB;  | Ch Similarity 40  1 Similarity 40  230, Conservative  10 GLLALLPPGAAS'  11 GLLSLARGSEVGNS  68 NASLSFLQDIQE  71 NADLSFLQMIREVTG  22 VLDNGDPLNNTTPVTV  19 VMLNYNT  82 NNQLALTLIDTNRSR  70 RDAEIVVKDNGR;  71 CCHEQCAAGCTGPKH;  72 CCHECCAGGCSGPQP   |
| Alternative SIGNAL CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN COOVAIN N BIND BIND BIND BIND BIND BIND BIND  | i i i   | itimil.  GLLLL  GLLLP  GLLP  GLLP  WASL  VLDN  VLDN  VLDN  VLDN  VLDN  CCHEC  CCCHEC  CCCCHEC  CCCHEC  CCCCHEC  CCCHEC  CCCHEC  CCCCHEC  CCCHEC  CCCHEC  CCCHEC  C |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE
BOWNIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES
AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF
PHOSPHATIDYLINGSITOL 3-KINASE.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE-Liver;
MEDLINE=9609635; PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
"Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
                            062759; 062955;
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(c-erbB3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; GlycoproteIn; Mulfigene family; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                            REVISIONS TO 85, 513 AND 565.
Hellyer N.J., Koland J.G.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                      PRT; 1339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCEPPO: IPRO00494; EGPR L domain.
InterPro: IPR000719; ENk pkinase.
InterPro: IPR001245; Furin-like.
InterPro: IPR001245; Tyr pkinase.
Pfam; PP00105; Pkinase; 1.
Pfam; PP001030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; ENk pkinase; 1.
SWART; SM00261; FU; 5.
                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U52530; AAC53050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U29339; AAC28498.2; -.
                      STANDARD;
                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                       Gene 165:279-284 (1995).
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxiD=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                     ERB3 RAT
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                                                                 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3
kinase; ATP-binding; Phosphorylation.
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SG--SRYQTVDSSNIDGFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVPRTVREI
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                                                TGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGL
                                                                 ALIHHNTHLCFVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPG
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13.AUG-1987 (Rel. 05, Created)
12.DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
(Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB).
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
                                                                                                                                                                                                                                reveals
                     Drosophila melanogaster (Fruit fly).
Nakaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoc
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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STRAIN-Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; PubMed=3093080;
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  TOP OR C-ERBB OR DER OR CG10079.
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                                                                                                                                                                            MEDLINE=94350209; PubMed=8070664;
Clifford R., Schupbach T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTER/OR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng T., Zhong K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for
the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perrimon N., Perkins L.A.; "There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYTOSINE PHOSPHATE.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                              MEDLINE=85137938; PubMed=2983232; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; M. Drosophila genomic sequence with homology to human epidermal growth factor receptor."; Nature 314:178-180(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF052754; AAC08536.1; -.
EMBL; AF052753; AAC08536.1; JOINED.
EMBL; AF052754; AAC08535.1; -.
EMBL; AF052752; AAC08535.1; JOINED.
EMBL; K03054; AAA31462.1; -.
EMBL; K03417; AAA51460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE=97248481; PubMed=9094709;
                                                                                                                                                                                                                             SEQUENCE OF 959-1078 FROM N.A.
                                                                                                                                                                                                                                                  STRAIN=Daekwanryeong
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DARAR REPRENTE PROCESS CONTROL OF THE PROCESS OF TH

REVIEW.

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100 KICIGTKSRLSVPSNKEHHYRNLRDRYTNCTYVDGNLKLTWLPNENLDLSFLDNIREV-- 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000494; EGFR L domain.

InterPro; IPR000494; EGFR L domain.

InterPro; IPR00019; Euk_pkīnase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR00103; Furin-like; 1.

InterPro; IPR00109; TyrKINASE.

INTERPROSITE; PR00109; TyrKINASE.

INTERPROSITE; PS00107; PROTEIN KINASE ATP; 1.

INTERPROSITE; PS0011; PROTEIN KINASE TYR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 NNFTVSFWLRVPKVSASHLEQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 ASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 32.5%; Pred. No. 6.98-95; noservative 185; Mismatches 436; Indels 344; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1919; DB 1; Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
AF109077; AAD26134.1; AF109078; AAD26132.1; AF109078; AAD26132.1; AF109089; AAD26133.1; AF109084; AAD26133.1; AF109089; AAD26133.1; AF109089; AAD26131.1; AF109089; AAD26131.1; AF109080; AAD26131.1; AF109080; AAD26131.1; AF109080; AAD26135.1; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; ABCU3434; AALTACE EMBL; X02293; CAA26157.1; ---
EMBL; X78918; CAA55523.1; ---
EMBL; X78919; CAA55521.1; ---
PMR, X78919; CAA55521.1; ---
PLR, A00640; GQFPE
HSSP; P11362; 1FGK.
F1YBase; FBGN0003731; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.0%;
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SIGNAL 1 30
CHAIN 31 1426
DOWAIN 31 869
TRANSMEM 869 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphate.

-!- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
THE INSERTION OF RETROVIED PROPUER ELEMENTS IN OR NEAR THE
C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                   15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
      1359 LNAOTLGVGESPIPTOTIGIPVMGGPGTMEVKVPMPGSEPTSSDHEYYND 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%; Score 1749.5; DB 1; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TYRKZ; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosing-protein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                    MEDLINE=85228222; PubMed=2988784; Nisen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Maroney P.A., Kung H. -J.; Crittenden L.B., M.A., Kung H. -J.; CerbB activation in ALV-induced erythroblastosis: novel moroesing and promoter insertion result in expression of amino-truncated EGF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E705E33A0BE01FCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rted. NO. 2.3e-86;
79; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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                                                                                      634 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M10066; AAA48763.1; ALT_INIT.
PIR; A00643; TVCHLV.
PIR; B00643; TVFVLV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P11362; 1FGK.
InterPro; 1PR000719; Buk pkinase.
InterPro; 1PR00145; Tyr pkinase.
Pfam; PF00069; pkinase; I.
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                                                                                                                   (Rel. 01, Created)
(Rel. 38, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70891 MW;
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                                                                                                                                                                                                        Avian leukosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 AA;
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Matches 370; Conser
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                   21-JUL-1986 (
15-JUL-1999 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593
                                                                                      ERBB ALV
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BINDING
                                                   RESULT 12
                                                                     ERBB ALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1190 LTTVFAEFARDPGRYLAIPGDKFTRLPA-----YTSQDEKDLIRKLAPTTDGSEAIAK 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1087 AGSDVFDG---DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQP 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LDLPVDEDDYLMP-TCOPGP 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : : | : : | : : | 1320 NNNNNMN------NPNQNNMAAVGVAAGYM------DLIGVPVSVDNPEYL 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1243 PDDYLQPKAAPGPS-----HRTDCT------DEMPKLNRYCKDPSNKNSS 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                        647
376 ACVRSCPQDKMDKGGE----CVPCNGPCPKTCPGVTVLH-----AGNIDSFRNCTV 422
                                                                                                                   LSVFQNLQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 486
                                                                                                                                                                                                                                                                                                                                                      655 PKNKYNDRGVCRECHATCDGCTGPKDTIGIGACTTCNLAIINNDATVKRCLLKDDKCPD-713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            857
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                                                                                                                                      543 RWPAIQKEPEÖKVWVNENLRADLCEKNGTICSDQCNEDGCWGAGTDQCLTCKNFNFNGTC
                                                                                                                                                                                                                                                                        603 IADCGYISNAYK--FDNRTCKICHPECR-----TCNGAGADHCQECVHVRDGQHCVSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990 YICRQKQKAKKETVKMTMALSGCEDSEPLRPSNIGANLCKLRIVKDAELRKGGVLGMGAF
                                                  IFGSLAFLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDSLPD
                                                                        PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
                                                                                                                                                                                                                                                   547 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                                                                        ----PDL
                                                                                                                                                                                                                                                                                                                                                                                                                      714 GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        772 ECPADHYTDEEQRECFQRHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNV
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                                                                                                                                                                                                                                                                                                                                                                                     615 SYMPIWKF--PDEEGACQP-----CPI---
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MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=79685;
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Debuirs B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Sayle S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals
new type of oncogene.";
Science 224:1456-1459(1984).
-I. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein
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Cell 35:71-78(1983).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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LYTOSINE PHOSPHATE.
DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
BENTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
IN CHICKENS.
MISCELLANBOUGS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE
MISCELLANBOUGS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R PIR; A00644; TVVUH.

R PIR; A00644; TVVUH.

R INCEPPO; IPRO0719; Euk_pkinase.

R IncerPro; IPRO01245; Tyr_pkinase.

R IncerPro; IPRO01245; Tyr_pkinase.

R Propom; PD000601; Euk_pkinase; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSITE; PS00119; PROTEIN KINASE DOM; 1.

R PROSITE; PS00119; PROTEIN KINASE DOM; 1.

R PROSITE; PS00119; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 604;
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ATP (BY SIMILARITY).
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R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
W, 76EBCDD06745D609 CRC64;
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YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1070

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Conservative
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                                                                                                                                      1126 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
                                                                                                                                                                                                                                1184 NGVVKDVFAF-----------GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD 1224
                                                                              1071 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.,
"A single amino acid substitution in v-erbB confers a thermolabile
phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 2.7.1.112)
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InterPro; IPR001245; Tyr pkinase.
Fram, PR00069; pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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    -NSPST--
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H -> D (IN THERMOLABILE V
5B53297AA068B65D CRC64;
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB
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ATP (BY SIMILARITY).
                                                                                                                                                                     FLEESIDDGFL-----PAPEYVNQ--LMPKKPSTAM-
                                                                                                                                                                                                                                                                                                                             NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian erythroblastosis virus (strain ts167)
                                                                                                                                                                                                                                                                                                                                                                         SSPYWIQSGNHQ-----INLDNPDY
418 YRTLMEEEDMEDIVDADEYLVPHQGFF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=87064458; PubMed=2878364;
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540 AA;
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Ullrich A., Vennstrom B., Schlessinger J., Givol D.;
Chicken epidermal growth factor (EGF) receptor: cDNA cloning,
expression in mouse cells, and differential binding of EGF and
transforming growth factor alpha.";
Mol. Cell. Biol. 8:1570-1978(1988).
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
                                                                                                                                                                                                                                                                                                            59 NGSKIPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELREATSPKANK
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                                                                                 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEO
                                                                                                                                                                                                                                                          653 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                                                                                                                                               CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCOLCHPNCTRGCKGPGLEGCP---
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gaps
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01-JAN-1990 (Rel. 13, Last sequence update)
15-UIN-2002 (Rel. 14. Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (CER)
Mismatches 119; Indels
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SEQUENCE FROM N.A.
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NCBI_TaxID=9031;
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                          DNA
                                                                          cell
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR00194; EGFR L domain.
R InterPro; IPR00179; Euk pkinase.
R InterPro; IPR0012174; Furin-like.
R InterPro; IPR0012174; Furin-like.
R Pfam; PF00100; Recep_L_domain; 2.
R MART; SM00261; FU; 4.
R PROSITE; PS001109; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS001109; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS001109; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS001109; PROTEIN KINASE DOM; PARTIAL.
R Transmembrane; Glycoprotein, Receptor; Signal; Transferase;
T Transmembrane; Glycoprotein, Receptor; Signal; Transferase;
T CHAIN 31 > 703 EPIDERMAL GROWTH FACTOR RECEPTOR.
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                                  SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANBOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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BY SIMILARITY.
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703 AA;
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296
                                                                                                                                          SEK-PLIVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPS 236
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                                                                                                                                                                                                                                                                                                                                                                                     355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLOVFETLEEITGYLYIS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTH 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597 KDPPPCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                596 IDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---NGSK 651
                                                                                                                   121
                                                                                                                                                                                                 VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 181
                                         61
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                                                                                                                                                                                                                                                                                                                                                          DCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGAAVLVLLLLGVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLE
                                                                                                                     LTYLPINASLSFLODIOEVOFNNFTVSFWLRVPKVSASHLEORLRIVRGTQLFEDNYALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 FIRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHY
                                       RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTP 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP 708
309; Conservative 115; Mismatches 255; Indels
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GenCore version 5.1.6
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protein search, using sw model • OM protein

Run on:

July 22, 2003, 08:22:34; Search time 48.5887 Seconds (without alignments) 5347.444 Million cell updates/sec

SEQ4-59-73-14 6847

Title: Perfect score:

1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\* sp\_bacteria:\* SPTREMBL Database

sp\_fungi:\*
sp\_human:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\*
sp\_phage:\*
sp\_rodent:\*
sp\_virus:\*
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sp\_virus:\* sp archeap:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description                   | O18735 canis famil | O9dx70 rattus norv | Q9ep98 mus musculu | O9wef6 gallus gall | O9yh40 xiphophorus | P79754 fugu rubrip | Q9bih9 anopheles q | Q9uk79 homo sapien | O8r2x1 mus musculu | 086712 avian rous- | 086714 avian rous- | O8wyv0 homo sapien | 064895 avian eryth | 085468 avian ervth | O9wvf5 mus musculu | Operv6 mus musculu |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES | ΩI                            | 018735             | 090X70             | Q9EP98             | Q9W6F6             | Q9YH40             | P79754             | 6нін60             | Q9UK79             | Q8R2X1             | 086712             | 086714             | Q8WYV0             | Q64895             | 085468             | Q9WVF5             | Q9ERV6             |
|           | DB                            | 9                  | 11                 | 11                 | 13                 | 13                 | 13                 | Ŋ                  | 4                  | 11                 | 15                 | 15                 | 4                  | 15                 | 15                 | 11                 | 11                 |
|           | %<br>Query<br>Match Length DB | 1259               | 1209               | 1210               | 1137               | 1165               | 1328               | 1433               | 419                | 367                | 729                | 567                | 412                | 962                | 545                | 655                | 643                |
|           | %<br>Query<br>Match           | 90.6               | 45.3               | 44.9               |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | 21.4               | 21.1               |
|           | Score                         | 6202               | 3101               | 3072               | 2729.5             | 2683               | 2263               | 1999.5             | 1775.5             | 1739               | 1720               | 1718               | 1697.5             | 1653.5             | 1645               | 1463.5             | 1447.5             |
|           | Result<br>No.                 | н                  | 7                  | m                  | 4                  | S                  | 9                  | 7                  | 80                 | σι                 | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |
|           |                               |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

| Q9y1x8 ephydatia f |         | Q26566 schistosoma | Q90836 gallus gall | Q9ese0 rattus norv | Q14256 homo sapien | Q9psh2 gallus gall | Q923v5 rattus norv | P11776 xiphophorus | O8szwl drosophila | Q9pvz4 xenopus lae | Q99162 xiphophorus | Q9njv5 biomphalari | Q9bg66 oryctolagus | O93457 scophthalmu | 073798 xenopus lae | Q8uw85 paralichthy | Q8uw86 paralichthy | Q9bud7 homo sapien | Q8uw84 paralichthy | Q8uw83 paralichthy | Q9qvw4 rattus sp. |        | Q9u5a8 bombyx mori | Q9vd94 drosophila | Q91ym0 mus musculu | Q96135 homo sapien | Q99mr2 mus musculu | Q07912 homo sapien |
|--------------------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| Q9Y1X8             | .023821 | Q26566             | 090836             | Q9ESE0             | 014256             | Q9PSH2             | Q923V5             | P11776             | Q8SZW1            | Q9PVZ4             | 099162             | Q9NJV5             | Q9BG66             | 093457             | 073798             | Q8UW85             | QBUW86             | Q9BUD7             | Q8UW84             | QBUWB3             | Q9QVW4            | Q9YGH8 | Q9U5A8             | Q9VD94            | Q91YM0             | Q96L35             | Q99MR2             | Q07912             |
| S                  | Ŋ       | Ŋ                  | 13                 | 11                 | 4                  | 13                 | 1                  | 13                 | Ŋ                 | 13                 | 13                 | Ŋ                  | 9                  | 13                 | 13                 | 13                 | 13                 | 4                  | 13                 | 13                 | 1                 | 13     | Ŋ                  | S                 | 11                 | 4                  | 11                 | 4                  |
| 1193               | 1368    | 1717               | 527                | 478                | 165                | 599                | 176                | 346                | 435               | 1362               | 311                | 1671               | 149                | 1418               | 1358               | 1368               | 1369               | 331                | 1412               | 1418               | 1371              | 1245   | 1472               | 2144              | 987                | 935                | 987                | 1036               |
| 18.5               | 17.1    | 16.4               | 15.9               | 14.2               | 13.2               | 13.2               | 13.0               | 11.8               | 11.4              | 11.1               | 11.0               | 10.7               | 10.6               | 10.4               | 10.3               | 10.3               | 9.9                | 6.6                | 9.6                | 9.7                | 9.6               | 9.4    | 9.4                | 0.6               | 8.8                | 8.8                | 8.8                | 9.8                |
| 1269               | 1172.5  | 1121               | 1086               | 973.5              | 906                | 902.5              | 887                | 806.5              | 778               | 757.5              | 754.5              | 732                | 723                | 712                | 106                | 702.5              | 678.5              | 919                | 668                | 667.5              | 658               | 645    | 643.5              | 617.5             | 604                | 603                | 601                | 587.5              |
| 17                 | 18      | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                | 27                 | 28                 | 59                 | 30                 | 31                 | 32                 | 33                 | 34                 | 32                 | 36                 | 37                 | 38                | 39     | 40                 | 41                | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

```
Canis familiaris (Dog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                        A TOCACHAIN TO TEXEL TO THE TOTAL TO THE TEXEL TEXEL TEXEL TO THE TEXEL T
                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ErbB-2.
                                                           PRT; 1259 AA.
                                                           PRELIMINARY;
                                                           018735
RESULT 1
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N

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1141 PQPEYVNOPDVRPOPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGG 1195
receptor is
                                                                    LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-FIGHBR, TISSUE=LIVER,
MEDLINE-9025688; PubMed-2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J.,
                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3101; DB 11;
Pred. No. 5.9e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Create 01-MAY-2000 (TrEMBLrel. 13, Last 8 01-JUN-2002 (TrEMBLrel. 21, Last 8 Epidermal growth factor receptor.
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STRAIN=FISHER; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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GLDVPV 1259
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Best Local Similarity
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                                                     MELAALCRWGILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                  1 MELAAWCKWGLLLALLPSGAAGTOVCTGTDMKLRLPASPETHLDMLRHLYOGCOVVOGNL
                                                                                                                                  ELTYLPTNASLSFLQDIQEVQFNNFTVSFWLRVPKVSASHLEQRLRIVRGTQLFEDNYAL
                                                                                                                                                                                                                                                               KNNQLALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTD
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                                      Gaps
                                    12;
      Length 1259;
                                   64; Indels
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9
      DB
     ; Score 6202; D
; Pred. No. 0;
42; Mismatches
     90.6%;
 Query Match
Best Local Similarity 90.7
Matches 1148; Conservative
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| QY         1076 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGY 1133           Db         1031 -SRTPLLSSLSANSNSSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTF 1085           QY         1134 VAPLTCSPQPETVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVKDVFAF 1193           Db         1086 LPVPEYINQ-SVPKRRPAGSVQNPVYHNQPLHPAPGRDLHYQNPH 1128           QY         1194 GGAVENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQAPGRDLHYQNPH 1128           QY         1129 SNAVSNPBYLNTAQPTCLSSGFDSSALWIQKGSHQMSLDNPDYQODFFPKE 1179           QY         1237 GAPPSTFKGTPTAENPEYLGLDVP 1260           Db         1180 AKPNGIFKG-PTAENAEYLRVAPP 1202 | PRESULT 3  OBERDA  AC OBERDA  AC OBERDA  DT 01-WAR-2001 (TERMELR-1] 16, Created)  DT 01-WAR-2001 (TERMELR-1] 16, Last sequence update)  DT 01-WAR-2001 (TERMELR-1] 16, Last sequence update)  BY 01-WAR-2001 (TERMELR-1] 16, Last sequence update)  ON 01-WAR-2001 (TERMELR-1] 16, Last sequence update)  ON DATE (TERMELR-1] 16, Last sequence and (TERMELR-1) 16, TERMELR-1, TERMERR-1, TERMER |
|---|--|
| Matchès 634; Conservative 169; Mismatches 359; Indels 122; Gaps 28;           Oy         3 LAALCRWGLLIALIPPGA-ASTQVCTGTDMKLRIPASPETHLDMLRHLYQGCQVVQGNLE 61           Db         15 LAALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRNFNNCEVVLGNLE 66           Oy         62 LTYLPTNASLSFLQDIQEVQ-FNNFTVSFWLRVPKVSASHLEQRLRIVRGTQLFEDNYAL 120           Oy         67 LTYLPTNASLSFLQDIQEVQ-FNNFTVSFWLRVPKVSASHLEQRLRIVRGTQLFEDNYAL 119           Oy         121 AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTFLLKGGVLIQRNPQLCYQDTLLWKDIFH 180           I  | THE CHECCHECCAGCTGPRESDCLACHFNHSGICELHCPALVIYNDTFESNIPPEGRYTEG SDCCHOQCAAGCTGPRESDCLACHFNHSGICELHCPALVIYNDTFESNIPPEGRYTEG SDCCHOQCAAGCTGPRESDCLACHFNHSGICELHCPALVIYNDTFESNIPPEGRYTEG SDCCHOQCAAGCTGPRESDCLACHPREBEATKDDTCPPLANTYVMDVPTGASFG ACCVKCCPRNYLYDGSCTACCPLINGEATELDESPDCDASCKCKCDGPCRKVCNGIGGERND VRAYTSANIGEPAGCKXIPGSLAFLPESPDCDPASNIAALDGPGLQVFFTLEEITGYLYI TLSINATNIKHFXYCTAISGLALLPANFEDESCASTRAPLOPRELEILKYVEHTGFLLIHNT SAMPDSLPDLSVFONLQVIRGRILHANRFEDESCASTRAPLOPRELILKYVEHTGFLLIHNT ACVARTSANIGEPAGCKXIPGGPSTAVARCHCPPECCACAGGGCCACAGFFLANT SAMPDSLPDLSVFONLQVIRGRILHANRFEDESCASTRAPLASGCGCAGFFFTGFLLIHNT ACVARTINAMKALFGTPROATTANRFEDESCASTRAPLASGCACAGFFACT NLCYANTINAMKALFGTPROATTANRFEDESCASTRAPLASGCACAGFFACT NLCYANTINAMKALFGTPROATTANRFEDESCASTRAPLASGCACAGFFACT NLCYANTINAMKALFGTPROATTANRFEDESCASTRAPLASGCACAGFFACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACT NLCYANTINAMKALFGTPROATTANRFEDESCACACAGFTACTACAGFTACTACAGFTACTACTACTAGGAGFTACTACTAGGAGFTACTACTAGGAGFTACTACTAGGAGFTACTAGGAG |

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LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLT 1138
                                                                                                                                                                                                                                                                                                             1139 CSPOPEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVE 1198
                                                                                                                                                                                                                                                                                                                                        --pvpeyvnq-svpkrppagsvqnpvyhnqplhp-----apgrdlhyqn--phsnavg 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                    1199 NPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPS 1241
890 HRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIM 949
                                                                                                                                                                              ----NSPST----SRTP
                                             VKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDM
                                                                                                                                   . 1021 GDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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MEDINE-99263203; PubMed=10328884;

MEDINE-99263203; PubMed=10328884;

MISTAIDHLOO of meuregulin-1 (nrg1) and erbB4 transcripts in embryonic chick hindbrain.";

MO1. Cell. Neurosci. 13:237-258(1999).

ENBL; AFLI363; AAD31764.1; -...

RINGERPTO; IPRO00494; EGFR L domain.

RINGERPTO; IPRO00194; EGFR L domain.

RINGERPTO; IPRO01304; FULTI-1ike.

RINGERPTO; IPRO01369; TWFR c6.

RINGERPTO; IPRO01269; TWFR c6.

REPEAR; PF001030; Recept L domain; 1.

R PÉam; PF001030; Recept L domain; 1.

R PÉam; PF001030; Recept L domain; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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ProDom; PRO01001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
                                                                                                                                                              1242 TFKGTPTAENPEYLGLDVP 1260
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|1186 IFKG-PTAENAEYLRVAPP 1203
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NCBI_TaxID=9031;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 NATNIKHFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 482
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                                                                                                                                                                                                                                                                                                                                                               74 YDLSFLKTIQEVAGYVLIALNTVERIPL-----ENLQIIRGNALYENTYALAILSN-- 124
                                                                                                                                                                                                                                                                                                                                                                                                                             PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YGINRIGLERELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNM 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 QLALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLIRIVCAGGCA-RCKGPLPIDCC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 HEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV 362
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                                                                                                                                                                                                                                                   LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                                                                                                                                                                                          Gaps
                                                                                                                                                            tch ' 44.9%; Score 3072; DB 11; Length 1210; al Similarity 48.9%; Pred. No. 9.3e-224; 625; Conservative 171; Mismatches 365; Indels 118;
  PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
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Best Local
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56 VQGNLELTYLPTNASLSFLQDIQEV-----QFNNFTVSFWLRVPKVSASHLEQRLRIVR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELLEL----LILLLISIGRCCSTDPDRKVCOGTSNOMTM----LDNHYLKMKKMYSGCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                              Xiphophorus xiphidiun.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R FÉAM, PPO0069, PAINASE, I.

R PÉAM, PPO0069, PAINASE, I.

R PRINTS, PRO10109, TYRKINASE.

R PRODOMS, PD000109, TYRKINASE.

R SMART, SM00261; FU, 3.

R SMART, SM00219; TYRK: I.

R PROSITE; PS00199, CYTOCHROME C, UNKNOWN I.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00109; PROTEIN KINASE TYR; I.

R ATP-binding; Kinase; Transferase; Tyrosine-protein Kinase.

SEQUENCE 1165 AA; 129614 MW; 7F7EB38D8771A74E CRC64;
    Duschl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RIO PURIFICATION;
MEDLINE=99241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., D
Dimitrijevic J., Schartl M.,
Altschmied J., Schartl M.,
Activation of the Yark proto-oncogene of Xiphophorus
overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.2%; Score 2683; DB 13;
ilarity 44.9%; Pred. No. 2.7e-194;
Conservative 164; Mismatches 385;
                                                                1213 PHPPPAFSPAFINLYYWDQDPPERGA--PPSTFKGTPT
                                                                                                                                                                                                                                                                                                               Receptor tyrosine kinase proto-oncogene.
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HSSP; P11362; 1FGK.
InterPro; IPR000345; CytC_heme_bind.
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR002174; Furin-like.
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InterPro, IPR001245; Tyr pkinase.
Pfam; PF00757; Furin-like; 1.
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                                                                                                                                                                                                           PRELIMINARY;
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STRAIN=RIO PURIFICATION;
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Schartl M.;
"---irred (JUL-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1162 PLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----AFGGAVENPEYLTPQGGAAPQ 1212
                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVIQNED-LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHH 1051
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                                                                                                                                                                                   QLEHNHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICP 179
                                                                                                                                                                                                                                                                                                                                RVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQV 405
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                                                                                                                       LCFADTIHWQDIVRNPWASNFTLVPTNGSSGCGRCHKSCTG-RCWGPTENHCQTLTKTVC
                                                                                                                                                              AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF
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                                          Gaps
39.9%; Score 2729.5; DB 13; Length 1137; 47.3%; Pred. No. 7.9e-198; ive 169; Mismatches 354; Indels 77;
                                        Conservative
                     Similarity
                                          539;
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SRPEYLNTNQNSL - - - PLVSSGSMDDPDY - - - QAG-
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HSSP; P11362; 1FGK.
INTERPRO; IPR000494; EGFR L domain.
INTERPRO; IPR000194; EUTIN-like.
INTERPRO; IPR00119; EUK pkknase.
INTERPRO; IPR00124; Tyr pkknase.
Pfam; PF00177; FVIIN-like; 1...
Pfam; PF00177; FVIIN-like; 1...
Pfam; PF00109; Recep L domain; 2...
Pfam; PF01010; Recep L domain; 2...
SWART; SM00261; FU; 3...
SWART; SM00261; FU; 3...
                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE=99177347; Pubmed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA a
                       1234 PERGAPPSTFKGTPTAENPEYLGL
                                          POTGALTGNGMFLPAAENLEYLGL
                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                     PRELIMINARY;
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                                                                                                                                       DNPNIKYTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVC 339
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                                                                                           CNRRCRGPKPIDCCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPPRIYDIVSHOVV
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                                                                                                                                                                                                                                                                                                                      ANCSKCAHFQDGPQCIPRCPHGMLGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSG
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-----RYKRIN-RQGS----
                                  QDTILLWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGG
                                                       162 VETÍNWADÍVDKTSNPTMALÍPHAPEROCOKODPGCVNGSCWAPGPGHCOKFTKLLCAEO
                                                                              C-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESM
                                                                                                                           PNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVC
                                                                                                                                                                      YGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFET
                                                                                                                                                                                           DGIGIGSLSNTIAVNSTNIGSFSNCTKINGDIILNRNSFEGDPHYKIGPMDPEHLWNLTT
                                                                                                                                                                                                                  LEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLREL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetraodontidae, Takifugu
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ATP-binding; Transferase
SEQUENCE 1328 AA; 148613 MW; A333039258B647E9 CRC64;
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Conservative 199; Mismatches 396;
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Anopheles gambiae (African malaria mosquito).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1433;
                                                                                                                                                                                                                                                                                           gambiae
                                                                                                                                                                                                                                                                          Tyloning expression and localisation of the Anopheles gambi epidermal growth factor receptor.";

Eudick (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ301655; CAG15008.1; --

EMBL; AJ301655; CAG15008.1; --

EMBL; AJ3010655; CAG15008.1; --

ENDISON IPRO00345; CFRL Ldomain.

InterPro; IPR000494; EGFL Ldomain.

InterPro; IPR000199; Buk pkinase.

EnterPro; IPR001297; Furin-like.

EnterPro; IPR001245; Tyr pkinase.

EnterPro; IPR00125; TYREINASE.

ENTERPROSITE; PR00109; TYREIN KINASE ATP; 1.

ENGSITE; PR00110; FROTEIN KINASE TYR; 1.

ENGSITE; PR00110; FROTEIN KINASE TYR; 1.
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1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1025 -----DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPR 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VEPS-DEMPK 1182
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                                       607
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DQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE 548
                                                 556 TTKHAMNGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLAKKDESCPDGY 615
                                                                                                                                      616 YSDYVLQEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQD 675
                                                                                                                                                         ----ACQPCPINCT-----HSCVDL-----DD-----KGCPAEQ--- 652
                                                                                                                                                                            676 FYANEETRICLPCHQECRGCHGLGDDHHECRNLKLFEGDPYDNATTFTCVSNCPASHPYK 735
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                                                                             -----SGVKPDLSYMPIWKFPD-- 624
                                                                                                                                                                                                SEIKKSSDHEVWVQXNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLD
                                       ECRVLQGLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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NTPNGMPTHQHSQ 1287
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419 AA

PRT;

PRELIMINARY;

Q9UK79 Q9UK79;

RESULT 8
Q9UK79
ID Q9UK

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CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH 180
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AR177761; AAD56009.2; ...
InterPro; IPR000494; EGFR L. domain.
InterPro; IPR00174; Furin-like.
Pfam; PF01030; Recep L. domain; 1.

SMART; SM00261; FU; I.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Hypothetical 40.2 kDa protein.
Buka musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi.
                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mamnalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1775.5; DB 4; Length 419;
Pred. No. 3.8e-126;
9; Mismatches 38; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45472 MW; FECIBE347E2D030C CRC64;
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                     Last sequence update)
Last annotation update)
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85.0%;
  13,
16,
21,
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Best Local Similarity 85.0°
Matches 340; Conservative
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                       autoinhibitor.
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PS00109; PROTEIN_KINASE_TYR; 1.
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      PROSITE;
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                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                               61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPORFVVIQNEDLGPSSPMDSTFYRSL 120
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                                                                                                                                                                                                                                                                 1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                               121 LEDDDMGELVDAEEYLVPQQGFFSPDPALGTGSTAHRRHSSSARSGGGELTLGLEPSEE
                                                                                                                                                                                                                                          895 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94203659; PubMed=8152791; MEDLINE=94203659; PubMed=8152791; Vennstrom B., Raymoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Beug H.; Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes with different transforming capacities."; Oncogene 9:1307-1320(1994).

EMBL, S69372; AAC60725.1; -.

HSSP; P03322; 1A6S.
                                                                                                                                                                                                       Gaps
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                                                                                                                                                               Length 367;
                                                                                                                                                                                                       33; Indels
                                       Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL, BC027080; AAH27080.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian rous-associated virus type 1.
Viruses; Retroid.viruses; Retroviridae; Alpharetrovirus
                                                                                                    11 protein.
367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                             25.4%; Score 1739; DB 11; 88.0%; Pred. No. 1.8e-123;
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InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF02813; Retro M; 1.
Probom; PD000001; Euk pkinase; 1.
PROSTIE; PS00107; PROTEIN KINASE ATP; 1.
PROSTIE; PS50011; PROTEIN_KINASE_DOM; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                  Matches 323; Conservative
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                                                                                                                                                                                Similarity
                  SEQUENCE FROM N.A.
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POLYPROTEIN.
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                                                                                                                       SEQUENCE
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Best Local
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994 VIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMYHHR 1052
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                                                                                                                                                                                                          634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 HRSSSTRSGGGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSL 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NSPST------RNGQCH 631
                                                                                                                                                                                                                                                              141 PEETATPKTGP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHP 197
                                                                                                                                                                                                                                                                                                                           693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      934 AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV 993
                                                                                                                                                                                                       575 PONGSVICEGPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPI
                                                                                                                                                                                                                                                                                                                           NCTHSCVDLEDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I PVA I KVLRENTSPKANKE I LDEAYVMAGVGSPYVSRLLGI CLTSTVOLVTOLMPYGCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHVRENRGRL;3SQDLLNWCMQ1AKGMSYLEDVRLVHRDLAARNVLVKSPNHVK1TDFGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                RRLLQETELVEPLTPSGAMPNQAQMR1LKETELRKVKVLGSGAFGTVYKGIW1PDGENVK
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                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
                                                                                                                                                Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVREDSFVQRYSSDPTGNFLEESIDDGFL-----PAPEYVNQ--LMPKKPS
                                                                                        Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian rous-associated virus type 1.
Viruses: Retroid viruses; Retroviridae; Alpharetrovirus
VCBI_TaxID=11950;
ATP-binding, Transferase, Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914EFE1D63 CRC64;
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Last annotation update)
                                                                                  / Match 25.1%; Score 1720; DB 15; Local Similarity 54.8%; Pred. No. 1.4e-121; nes 358; Conservative 75; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Æ
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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PRELIMINARY;
          Homo sapiens (Human)
                                                   [1]
SEQUENCE FROM N.A.
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                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 643
                                                                                                                                                                                                                                                 702
                                                                                                                                                                                                                                                            ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 822
                                                                                                                                                                                                                                                                                                                                            YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 942
                                                                                                                                                                                                                                                                                                                                                                                                                            294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 KGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKMARDPPRYLVIQGDERMH 413
                                                                                                                                                                                                                                                                                          VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------- 454
                                                                                                                                                                                                                     544 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                         LGSQDLLNWCMQ1AKGMSYLEDVRLVHRDLAARNVLVKSPNHVK1TDFGLARLLDIDETE
                                                                                                                                                               25.1%; Score 1718; DB 15; Length 567; 55.4%; Pred. No. 1.3e-121; indels 102.
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                                                                                                                                            567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
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O1-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 LPSPIDSKFYRTLMEEEDMEDIVDADEXLVPHQGFF----
                           InterPro; IPR000719; Euk pkinase.
InterPro; IPR01245; Tyr pkinase.
Ptan; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1.
SWART; SW00219; TYRKC; 1
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYP; 1.
TYROSING-PROTEIN KINASE TYP; 1.
TYROSING-PROTEIN KINASE TYP; 1.
                                                                                            - - -
Oncogene 9:1307-1320(1994).
EMBL; S69372; AAC60727.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                           Best Local Simitarry .... Matches 357; Conservative
                                                                                                                                                                          Similarity
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SEQUENCE
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LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 895 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT 954
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, v-erb.A, v-erb.B protein.
GAG, V-ERB.A, V-ERB.B.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T., Wan D.F., Gu J.R., "Novel human cDNA clones with function of inhibiting cancer cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL, AF318349; AAL55856.1; -. interPro; IPR002048; EF-hand. InterPro; IPR00179; EW. pkinase. InterPro; IPR001245; Tyr pkinase. InterPro; IPR001245; Tyr pkinase. InterPro; IPR001049; YLP_motif.
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SMART; SM00219; TyrKc; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
SEQUENCE (all protein.
SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.8%; Score 1697.5; DB Best Local Similarity 80.5%; Pred. No. 3e-120; Matches 330; Conservative 5; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
Pfam; PF02757; YLP; 2.
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HRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP 1112
                                                                                                                                                                                                                                       ------PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLT 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88277326; PubMed=2897102; Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.; Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.; "Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation."; Oncogene Res. 1:265-278(1987).

EMBL; X06943; CAA30024.1; -.

EMBL; P1362; 1FGK.

InterPro; IPR000719; Buk pkinase.

InterPro; IPR001245; Tyr pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLQRYSEDPT'VPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GP -- DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEPLTPSGAMPNOAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 02, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyYKG; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR, 1.
ATP-binding; Transferase; TyTosine-protein kinase.
SEQUENCE 545 AA; 60899 WW; 140DCE8CCA0F8AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%; Score 1645; DB 15;
54.9%; Pred. No. 4.3e-116;
ive 70; Mismatches 121;
                                                                                                           -----SRTPLLSSLSATSN-
                                                                                                                                                                                                                                                                                                  -LERAKTLSPCKNGVVKDVFAFGGAVENPEYL 1203
                                                                                                                                                                                                                                                                                                                                   Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PONGSVTCFGPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIP 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRLLQERELVEPLTPSGEAPNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVT 581
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                                Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R. "Six amino acids from the retroviral gene gag greatly enhance th transforming potential of the oncogene V-erb-B."; Oncogene 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. EMBL; X52201; CAA36459.1; -.
EMBL; X52201; CAA36459.1; -.
EMBL; X52211; CAA36459.1; -.
HSSP; P10828; ZNLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00219; TyrKc; 1.

SWART; SM00319; TyrKc; 1.

SWART; SM00399; ZnF C4; 1.

PROSITE; PS00101; NUCLEAR RECEPTOR; 1.

PROSITE; PS50011; PROTEIN KINASE APP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS500109; PROTEIN KINASE TYR; 1.

ATP-binding; DNA-binding; Woclear procein; Keceptor; Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.1%; Score 1653.5; DB 15; Length 962; 51.7%; Pred. No. 2.3e-116; ive 73; Mismatches 142; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 VEECRVLQGLPRE-YVNAR-HCLP------
                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Buk_pkinase.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001485; Tyr_pkinase.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000001; Buk pkinase; 1.
ProDom; PD000035; Znf C4steroid; 1.
SWART; SM00430; HOLI; 1.
MEDLINE=90206603; PubMed=1969616;
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nes 358; Conservative
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                                                                                                                                                PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061
                                                                                                                                                                                                                                                                                            GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQ 1116
KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 1001
                                     Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
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Sciurognathi; Muridae; Murinae; Mus.
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Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balagubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse alternative Egfr transcripts encoding truncated receptor
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria; Rodentia;
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynskaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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R EMBL; ARC04944; ...

DR EMBL; ARC04911; BAB2365.1; ...

DR MGJ; MGG195294; BGFR.1; ...

DR InterPro; IPR000494; EGFR.1 domain.

DR InterPro; IPR00174; Furin-like.

DR Ffam; PF00757; Furin-like, 1.

Pfam; PF01030; Recep i_domain; 2.

"WART; SM00261; FU; 3.

"AA, 72906 MW; 6B;
                                                                                                                                                                                                                  EMBL; AF275366; AAC28047.1; -.
EMBL; AF275364; AAG28047.1; JOINED.
EMBL; AF275365; AAG28047.1; JOINED.
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July 22, 2003, 08:11:38; Search time 38.1589 Seconds (without alignments) 4403.399 Million cell updates/sec
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1 MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEXLGLDVPV 1261
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|   |        | Description     | Human herequlin 2 | Human tyrosine kin | HER2 transgene pla | Human HER2 (ErbB2) | HER-2/neu protein. | Human HER-2/neu on | Human HER-2/neu pr | Amino acid sequenc | Human HER-2/neu pr | HER2/neu amino aci |
|---|--------|-----------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   | ;      | ID              | AAY92620          | AAE12130           | AAB60167           | AAU74545           | AAWO1111           | AAW92406           | AAB21198           | AAY84780           | AAB85458           | AAG88267           |
|   |        | DB              | 21                | 22                 | 22                 | 23                 | 17                 | 50                 | 21                 | 21                 | 22                 | 22                 |
|   | •      | Watch Length DB | 1255              | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               |
| ф | Query  | Match           | 98.0              | 98.0               | 98.0               | 98.0               | 98.0               | 98.0               | 98.0               | 98.0               | 98.0               | 98.0               |
|   | ,      | Score           | 6713              | 6713               | 6713               | 6713               | 6707               | 6707               | 6707               | 6707               | 6707               | 6707               |
|   | Result | 0               | 1                 | 7                  | m                  | 4                  | Ŋ                  | 9                  | 7                  | 80                 | σ                  | 10                 |

| Her-2 prot<br>Her-2/neu | r-2/n<br>r-2/n | Sequence of c-erbB<br>Human breast cance | HER-2/n  | Rat HER-2/neu prot | Rat Her-2/neu onco | Mouse Her-2/neu pr | Amino acid sequenc |          | Human HER-2/neu fu | Her-2/neu extracel | Mouse Her-2/neu ex | Mouse Her-2/neu ex | Human HER-2/neu fu | Her-2/neu extracel | Her2-GM-CSF immuno | Extracellular HER- | Human Her-2/neu on | Human ErbB2 oncopr | Human ErbB2 extrac | DC8scFv-erbB2EC fu |          | Amino acid sequenc | Human EGF receptor | Human Her-1 protei | epide | Amino acid sequenc |          | Human protein for |          | Human protein for | Human epidermal gr |
|-------------------------|----------------|--|----------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|-------|--------------------|----------|-------------------|----------|-------------------|--------------------|
| AAE24067<br>AAE20479    | 11             | AAR39568<br>AAI198923                    | AAB21208 | σ                  | AAM51144           | AAB21206           | AAG62860           | AAM51151 | AAB21203           | AAM51148           | AAM51152           | AAM51153           | AAB21204           | AAM51149           | AAW19764           | AAB21200           | AAM51145           | AAB60408           | AAB61593           | AAY44993           | AAR08222 | AAB19259           | AAY50616           | AAE23019           | 9     | AAB68420           | AAE20483 | AAE20481          | AAE20484 | <b>E204</b>       | ABP51768           |
| 23                      | 23.3           | 14<br>2,                                 | 21       | 21                 | 23                 | 21                 | 22                 | 23       | 21                 | 23                 | 23                 | 23                 | 21                 | 23                 | 18                 | 21                 | 23                 | 22                 | 22                 | 21                 | Ξ        | 21                 | 21                 | 23                 | 23    | 22                 | 23       | 23                | 23       | 23                | 23                 |
| 1255                    | 1255           | 1433                                     | 1200     | 1256               | 1256               | 1256               | 1256               | 1256     | 919                | 919                | 920                | 926                | 712                | 712                | 782                | 653                | 653                | 645                | 645                | 951                | 624      | 1210               | 1210               | 1210               | 1210  | 1210               | 583      | 587               | 589      | 9                 | 1.210              |
| 0.88                    | 988            | 97.3                                     | 93.3     | 86.3               | 86.3               | 86.0               | 86.0               | 86.0     | 70.0               | 70.0               | 29.0               | 59.0               | 53.7               | 53.7               | 51.6               | 51.5               | 51.5               | 51.0               | 51.0               | 50.0               | 48.5     | 45.2               | 45.2               | 45.2               | 45.2  | 45.2               | 45.0     | 45.0              | 45.0     | 45.0              | 44.6               |
| 6707                    | 6707           |  | 6390     | σ                  | 5911.5             | œ                  | œ                  | œ        | 4793               | 4793               | 0                  | 4041.5             | 3677               | 3677               | 3531               | 3529               | 3529               | 3491               | 3491               | 3426               | 3323     | 3098               | 3098               | 3098               | 3098  | 3096               | 3084     | 3084              | 3083     | 3083              | 3057               |
| . 11                    | 1 T            | 15                                       | 17       | 18                 | 19                 | 20                 | 21                 | 22       | 23                 | 24                 | 25                 | 26                 | 2.7                | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35       | 36                 | 37                 | 38                 | 39    | 40                 | 41       | 42                | 43       | 44                | 45                 |

# ALIGNMENTS

|                      |                                      |   |           |   |                    |   |                           |   | e immunity;                            |   |   |   |          |   |                     |        |                    |                             |        |    | insertion"                                      |        |                          | insertion"                                      |        |                          | insertion"                                      |        |                          | insertion"                   |          |
|----------------------|--------------------------------------|---|-----------|---|--------------------|---|---------------------------|---|--|---|---|---|----------|---|---------------------|--------|--------------------|-----------------------------|--------|----|---|--------|--------------------------|---|--------|--------------------------|---|--------|--------------------------|------------------------------|----------|
|                      |                                      |   |           |   |                    |   |                           |   | lymphocyt                              | cancer;   | cope.   | 1 |          |   |                     |        |                    |                             |        |    | epitope   | 1      |                          | epitope   | ,      |                          | epitope   |        |                          | epitope                      |          |
|                      | AAY92620 standard; Frotein; 1255 AA. |   | 0;        |   | 2000 (first entry) |   | Human heregulin 2 (Her2). |   | in 2; Her2; vaccination; cytotoxic T-1 | self-protein; cancer; breast cancer; prostate cancer; | cell-associated peptide antigen; foreign epitope. |   | sapiens. |   | Location/Qualifiers | 1173   | /label= N-terminal | /note= "mature polypeptide" | 525    | ä  | /note= "suitable For foreign epitope insertion" | 5973   | /label= insertion region | /note= "suitable For foreign epitope insertion" | 103117 | /label= insertion region | /note= "suitable For foreign epitope insertion" | 149163 | /label= insertion_region | /note= "suitable for foreign | 174.,323 |
| RESULT 1<br>AAY92620 | AAY9262                              |   | AAY92620; |   | 10-AUG-2000        |   | Human h                   |   | Heregul                                | self-pr   | cell-as   |   | Homo sa  |   | Key                 | Domain |                    |                             | Region |    |   | Region |                          |   | Region |                          |   | Region |                          |                              | Domain   |
| RESU<br>AAY9         | ID                                   | X | AC        | × | DI                 | × | OE                        | × | Š                                      | ¥   | ¥   | × | os       | × | FH                  | FT     | FŦ                 | F                           | FT     | FT | FT  | FT     | FŢ                       | FT  | FŦ     | F                        | F   | FT     | ΕŢ                       | FT                           | Η        |

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Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the human heregulin 2 (Her2) sequence. Immunogenic analogues Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper egitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
      210..224
/label= insertion region
/note= "suitable For foreign epitope insertion"
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|abel= insertion region
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'note= "suitable for foreign epitope insertion"
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                                                                                      Ligand_binding_domain
                                                                                                                                                                         label= insertion region
note= "suitable for foreign
Cysteine_rich_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= C-terminal_domain
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lirk P, Karlsson G;
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98US-0105011
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 B-cell group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least ne foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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Pred. No. 0;
4; Mismatches
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Best Local Similarity 98.5%;
Matches 1242; Conservative 4
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (WHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful contentants of anti-cancer vaccines immunotherapy. They are useful as components of anti-cancer vaccines immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polymucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polymucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
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                                                                                                                           The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HER and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers
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                             AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to treating a tumour in a mammal, where the tumour receptor (ErbB) and does not respond or responds poolty, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, pepthelial, stromal, blastoccelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                                                                                                                                       Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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4; Mismatches
Sliwkowski M;
                                                                                                                                                                                                                                                                                                              English.
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Matches 1242; Conservative
                                                                                                                                                                                                                                                                                                                     Example 3; Fig 7; 93pp;
Schwall R,
                                                                 WPI; 2002-163686/21
N-PSDB; ABK14058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                              Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                                                           DNA encoding HER-2-neu poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/neu oncogene is
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1255
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                                                                                                                                                                                                                    Claim 2; Page 56-61; 71pp; English
                               95US-0414417.
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Matches 1240; Conservative
                                                          (UNIW ) UNIV WASHINGTON
                                                                                       Disis ML;
                                                                                                                  WPI; 1996-455361/45.
N-PSDB; AAT40739.
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   28-MAR-1996;
                              31-MAR-1995;
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                                                                                                      LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
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                                                                                                                                                                             AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLMWCMQIAKGMS
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/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
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breast cancer; prostate cancer; ovarian cancer; lung cancer;
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      FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                      VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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                                                                                                                                                                                                                                                                                                      The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
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                                                                                                                                                   acid encoding an erbB 2 receptor protein designated SPLICE inhibitors of the protein are useful for treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%; Score 6707; DB 21;
llarity 98.3%; Pred. No. 0;
Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                  Claim 3; Fig 2; 60pp; English.
Μď
                                                          WPI; 2000-303768/26.
N-PSDB; AAA14812.
Siegel.
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Matches 1240; Conserv
                                                                                                                                                      Nucleic acid
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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2).
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                                                                                    New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
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98.3%; Pred. No. 0;
iive 5; Mismatches
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 Hand-Zimmermann
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                                                                     LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
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                                                                                                                                                                                                             YLEDVRLUHRDILAARNYLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESI
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LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                            GDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                                                                                                                                                                                                                                                                                                          LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
                                   AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
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Keogh E;
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The present invention describes isolated prepared HER2/neu epitopes (I).

Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

culture in vitro and binds to a complex of an epitope (I), bound to a

human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

caids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (III) comprising (II) and a pharmaceutical

excipient; (4) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic

and immunostimulant activities, and can be used in vaccines (I), (II)

and (III) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (I) and (II) are useful for

complexity and treatment of cancer. (I) and (II) are useful for

antigen when incubated with a T lymphocyte smalle form a patient and

detecting the presence of bound T lymphocyte to (I) or (II). Epitope

based vaccines mean that immunosuppressive epitopes that may be present

complexity. The possible pathological side effects caused by

infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG88121 represent amino acid sequences used in the exemplification of the present invention. AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH 180 174 CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 360 ELTYLPTNASLSFLQDIQEVQFNNFTVSFWLRVPKVSASHLEQRLRIVRGTQLFEDNYAL 120 KNNQLALTLID'INRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTD 240 234 CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 300 420 CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 294 CVTACPYNYLS:TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 354 9 9 An isolated prepared  ${\tt HER2/neu}$  epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer-MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH KNNQLALTLIDTINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTD 1 MELAALCRWGLULALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL AVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA Gaps. . 9 Length 1255; Indels 98.0%; Score 6707; DB 22; 98.3%; Pred. No. 0; 10; 5; Mismatches Disclosure; Page 15; 199pp; English. Conservative 1255 AA; Best Local Similarity Matches 1240; Conserv 61 121 115 181 175 241 235 295 361 355 Sequence 301 Query Match ઠે В ò 9 ò g ð g ò 8 ò 셤 ò P

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WPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHL 474

CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF

WPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHL

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                                                                                              Cowsert
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N-PSDB; AAD38904.
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Best Local Similarity
Matches 1240; Conserv
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                                                                                             Bennett CF,
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CFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
                       LRGOECVEECRVLOGLPREYVNARHCLPCHPECOPONGSVTCFGPEADQCVACAHYKDPP
                                       LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                   VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                                                                                 LKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVM
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                                                                      FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                                                    FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
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  Human
                                                                                                                                                        The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative diseases or e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 WPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNNTHL
Novel antisense oligonucleotide which modulates the expression of Huma
Epidermal Growth Factor receptor, Her2, is useful for treating tumors
inflammation or to prevent infection in humans -
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
                   14-AUG-2001; 2001WO-US41733
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Mcneill PD, Vedvick TS;
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/note= "Naturally processed HLA-B44-restricted epitope"
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MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM
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                          FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                        FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                              VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                        LKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVM
                                                                                                                                    AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
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human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
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effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for leukcoyte antigen (HLA)-1844 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a human patient. The invention is useful for stimulating a T cell response in a human patient as probe or primer for notcleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full centire Her-2/Neu gene or gene fragments of interest, to isolate a full contractive in appropriate host cells. The composition is useful in propriate contractions and for the treatment of cancer, and propriate contractions and for the treatment of cancer, and propriate in appropriate applications and for the treatment of cancer, and propriate in a propriate applications and for the treatment of cancer, and propriate in a propriate applications and for the treatment of cancer, and propriate in a propriate applications and for the treatment of cancer, and propriate applications and for the treatment of cancer, and an appropriate applications and for the treatment of cancer, and a propriate applications and for the treatment of cancer, and an appropriate applications and for the treatment of cancer, and a propriate applications and for the treatment of cancer, and a propriate applications and for the treatment of cancer, and a propriate applications and for the cancer, and a propriate applications and for the cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human Her-2/neu protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated Her-2/Neu polypeptide composition
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Cheever MA,
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Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185; tyrosine kinase; receptor; c-erbB2; gene therapy.

/note= "phosphorylation domain"

/note= "intracellular 990..1255

. /note= "extracellular domain"

Location/Qualifiers

Homo sapiens

Domain Domain

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Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or

Claim 68; Fig 7; 141pp; English.

phosphorylation domain

CORIXA CORP. SMITHKLINE BEECHAM BIOLOGICALS.

(CORI-)

Cheever MA, Gheysen D;

WPI; 2002-241743/29

N-PSDB; ABA92250

03-AUG-2001; 2001WO-US24283. 03-AUG-2000; 2000US-0632507.

40200212341-A2

14-FEB-2002

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The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor commin with homology to the epidermal growth factor receptor intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and overian cancers. The invention provides Her-2/neu fusion proteins or nucleic acid modecules. In preferred fusion proteins or nucleic acid modecules. In preferred fusion proteins, the extracellular domain or protein is fused to a Her-2/neu intracellular domain or proposition domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by response to Her-2/neu protein is elicited or enhanced by crossing the fusion protein is elicited or enhanced by crossing the fusion protein is elicited or enhanced by crossing the fusion protein is elicited or enhanced by crossing the fusion protein and elivering the development of a cancer in a patient. The Husion proteins, nucleic acidic and isolated specific T-cells are useful for inhibiting the development of a cancer in a patient. The cells that specifically react with a Her-2/neu fusion proteins cancer in a patient.
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Human Her-2/neu oncogene-encoded p185 glycoprotein.

17,-JUN-2002

XEXEXEX

AAM51143

AAM51143 standard; Protein; 1255 AA.

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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Z/neu or a polypucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomes, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-Z/neu polypeptide.
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  EYLTPQGGAAFQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
                                                            EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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llarity 98.3%; Pred. No. 0;
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28-SEP-2000; 2000US-0675904.
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                         EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). X in AAR39583 represents the location of a stop codon in AAQ46083.
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7; Mismatches 15;
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llarity 97.8%;
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Matches 1233; Conserv
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                                     AVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH
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| ure 309, 270-273, 1984<br>itle: ATP-stimulated interaction between epidermal growth factor receptor and superco<br>eference number: A38023; MUID:84191554; PMID:6325948  | Db 532 GRECVDKCKLLEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHC 591 Qy 597 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656  |
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| ontents: annotation; receptor activity often the SGF receptor (and other tyrosine kinases) can nick double-stranded DNA hen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.  |  |
| 1 59, 33-43, 1989  'itle: Functional independence of the epidermal growth factor receptor from a domain geference number: A3331, MUID: 900003233, PMID: 2790960  | Qy 657 AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMR 713<br>   |
| Concerns: annotation; internativation signal comments annotation of the EGF-receptor dienetics: enetics:   | QY         714 ILKETELEKKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYV 773           Dh         706 II.KEPEPKYTKULGGABGHVKIMILGENVKIMIDEGENVKITONAIKEI.DEANV 765   |
| , 04   | 774 PAGCESPY/SELECTISTYOL/VTOLMPYCCLLDHYERREGEGGODLING/MONOING |
| eywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorotein; phos | 766 MASUDNEHUCRLIGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGM   |
| 5-1410/Froduct: Edr receptor #status predicted <mat> 5-645/Domain: extracellular #status predicted <ext> 5-300/Domain: EGF receptor extracellular domain repeat <eei> 600.600/Domain: EGF receptor extracellular domain repeat <eei></eei></eei></ext></mat>   | OY 834 SYLEDVRLYHRDLAARNVLYKSPNHYKITDFGLARLLDIDETBYHADGGKVPIKKMALES 893<br>  |
| 5.000/Domain: but receptor extracellular domain repeat.<br>9-1210/Domain: intracellular #status predicted <int><br/>0-975/Domain: protein kinase homology <kin></kin></int>  | OY 894 ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM 953  |
| 18-726/Region: protein kinase ATP-binding motif<br>99-1046/Region: coated pit mediated internalization signal  |  |
| 04/-1210/Region: inibicory<br>28,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic<br>45/Active site: Lys #status experimental  | Db 946 IMVKCWMIDADSRPKFRELIIEFSKWARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEE 1005   |
| atch<br>cal Similarity 49.1%; Pred. No. 9.6e-121;  | QY         1013 DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPR 1072  |
| acches 525; Conservative 1/8; mismacches 344; indeis 128; Gaps 22; 11 LLIALLPPGAASTQVCTFNNFTVSFWLRVPKVSASHLELYQGCQVVQ 57   | QY 1073 SPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP 1130  |
| 14 LLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVL 62<br>58 GNLELTYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVL 117   | 1131 LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA  |
| 63 GNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNMYYENSYALAVL 122  | 1088PVPEYINQ-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTA   |
| 118 DNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNN 177   | VENEZIL-INQCOMARQEREFARSEAFUNLIMUQ   |
| ILIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCC 23  | Oy 1234 PSTFKGTPTAENPEYL 1249  Db 1184 NGIFKGS-TAENAEYL 1198   |
| 237 HEOCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV 296   | RESULT 5<br>A33183<br>epidermal growth factor receptor precursor - mouse   |
| 297 TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV 356 293 KKCPRNYVVTDHGSCVRACGADSYEM-EEDGVRKCKKCGGPCRKVCNGIGIGGFKDSLSI 351  | C;Spectes: Mus musculus (house mouse)<br>C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999<br>C;Accession: A53183; A43818; Z24942; A28941; S45325; I49543<br>R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;   |
| 357 TSANIQEPAGCKKIFGSLAFLPESFDGDPASNTAPLQEBCLQVFETLEEITGYLYISAWP 416 :   | Genes Dev. 8, 393-413, 1994 A.Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor A.Reference number: A53183; MUID:94170986; PMID:8125255 A.Accession: A53183   |
| 417 DSLPDLSVFQNLQVIRGRILHNGAYSLTLGGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 ::  | A;Nolecule type: mkNA<br>A;Residues: 1-1210<br>A;Cross-references: GB:U03425<br>R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.  |
| 477 VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 536   | Oncogene 6, 673-676, 1991<br>A,Title: Comparison of EGF receptor sequences as a guide to study the ligand binding si<br>A,Reference number: A43818; WUID:91232866; PMID:2030916<br>A,Accession: A43818   |
| 537 GQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFC 596   | A,Molecule type: mRNA<br>A,Residues: 1-714 <avi><br/>A,Cross-references: GB:X59698</avi>   |

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| OY  353 VRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYI 412  Db  348 TLSINATNIKHFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLI 407  413 SAMPDSLPDLSVFONLQVIRGRILHNGAYSLTLQGLGISKLGLRSLREEGSGLALIHNT 472   | Oy 533 QFLRGGECVEECRVLQGLPREYUNARHCLPCHPECOPONGSVTCFGPEADQCVACAHYKD 592  Db 528 NVSRGRECVEKCNILEGEPREFVENSECIOCHPECLPQAMNITCTGRGPDNCIQCAHYID 587  Oy 593 PPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLT 652  | Qy         772 YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAK 831           Db         766 YVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDTVREHKDNIGSQYLLNWCVQIAK 825           Qy         832 GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEXHADGGKVPIKWMAL 891           Db         826 GMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMAL 895           CA         892 ESILRRRFTHQSDVWSYGVTVWELWTFQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMAL 885           CA         894 ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGBRLPQPPICTIDV 945           CA         896 ESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGBRLPQPPICTIDV 945           CA         897 ESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGBRLPQPPICTIDV 945           CA         898 ESILHRIYTHQSDVRSYGVTVWELMTFGSKPYDGIPASDISSILEKGBRLPQPPICTIDV 945           CA         898 ESILHRIYTHQSDVRSYGVTVWELMTFGSKPYDGIPASDISSILEKGBRLPQPPICTIDV 945           CA         898 ESILHRIYTHQSDVRSYGVTVWELMTFGSKPYDGIPASDISSILEKGBRLPQPPICTIDV 945           CA         898 ESILHRIYTHQSDVRSYGVTVWELMTFGSKPYDGIPASPLDSTFYRSLLE 1010           CA         898 ESILHRIYTHQSDVRSYGVTVWELMTFGSKPYDGIPASPLDSTFYRSLLE 1010 | OY 1011 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA 1070  1.  | RESULT 6  TVCHLV  polidermal growth factor receptor precursor - chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Accession: A27720; A00643 |
|---|--|---|--|--|
| RiBisinger, D.P.; Serrero, G. A.Reference number: \$24942 A.Reference number: \$24942 A.Reference number: \$24942 A.Reference number: \$24942 A.Roclecule type: mRNA A.Residues: \$69-971, 'K', 973-1115,'D' <eis> A.Roclecule type: mRNA A.Residues: \$69-971, 'K', 973-1115,'D' <eis> A.Reference number: \$63, 1315-13159, 1988 A.Ritleis Epidermal growth factor receptor threonine and serine residues phosphorylated in A.Reference number: A28941; MUID:88330814; PMID:3138233</eis></eis></eis></eis></eis></eis> | lie type: profession of the epidermal growth Factor Receptor S45325 si preliminary le type: UNA si plans, A.R.; Alexander, W.S. AL.; Dunn, A.R.; Alexander, W.S. AL.; Dunn, A.R.; Alexander, W.S. ed to the EMBL Data Library, April 1994 ption: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor ance number: S45325 siperiminary le type: UNA le type: UNA lestyle: UNA lestyle: UNA lestyle: UNA lestyle: UNA lestyle: UNA lestyle type: UNA lestyle: UNA lestyle: UNA lestyle: USA: ON 55-59, 1993 att. Acad. Sci. U.S.A. 90, 55-59, 1993 in Expression of the epidermal growth factor receptor gene is regulated in mouse becommeder: 149643; MUID:93126380; PMID:7678348 | A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 12-20,22-132 A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201 C;Gene: EGFR C;Gupericanily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro F;712-977/Domain: protein kinase homology < KIN> F;712-977/Domain: protein kinase ATP-binding motif F;680,695/Binding site: phosphate (fhr) (covalent) #status experimental F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental F;993/Binding site: (or 1937) phosphate (Ser) (covalent) #status experimental F;1028/Binding site: phosphate (Ser) (covalent) #status experimental F;1028/Binding site: phosphate (Ser) (covalent) #status experimental   | Query Match  45.7%; Score 3111; DB 2; Length 1210;  Best Local Similarity 49.1%; Pred. No. 6.98-120;  ILLIALLEPEGAASTQVCTFNNFTVSFWLRVPRVSASHLELXQGCQVVQ 57 | 233 TDCCHEQCAAGCTGPKHSDCIACLHFNHSGICELHCPALVTYNTDTFESMPNPBGRYTFG 292   |

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|---|--|--|--|
| Rilax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstr Wol. Cell. Biol. 8, 1970-1978, 1988 A.Title: Chicken epidermal Loyenth factor (BGF) receptor: CDNA cloning, expression in mou A; Reference number: A27720; MUID:88261272; PMID:3260329 A, Accession: A27720 A, Mocedule type: mRNA A, Residues: 1-1223 < LAX> A, Cross. references: GB:M20386 A, Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A, Residues: 585-1223 < LUB: Raines, M A; Reference number: A00643 A, Molecule type: mRNA A, Residues: 585-1223 < NIL> A, Molecule type: mRNA A, Residues: 585-1223 < NIL> A, Molecule type: mRNA A, Residues: 585-1223 < NIL> A, Gonetics: C, Genetics: C, Genetics: C, Genetics: GB:M10066 C, Genetics: C, Cometics: GB:M10066 C, Genetics: C, Cometics: GB:M10066 C, Genetics: C, Cometics: GB:M10066 C, Gonetics: C, Cometics: GB:M10066 C, Gonetics: C, Cometics: GB:M10066 C, Gonetics: C, | F;31-654/Domain: extracellular #status predicted <ext> F;81-507/Domain: EGF receptor extracellular domain repeat <ee1> F;81-307/Domain: EGF receptor extracellular domain repeat <ee2> F;87-10.00main: EGF receptor extracellular domain repeat <ee2> F;655-677/Domain: transmembrane #status predicted <tmm> F;678-123.70cmain: intracellular #status predicted <tmm> F;719-984/Domain: intracellular #status predicted <tmn> F;719-984/Domain: protein kinase homology <kin> F;727-735/Region: protein kinase ATP-binding motif F;136.202.809.361.730,422.575,580,615.535/Binding site: carbohydrate (Thr) (covalent) #status predicted F;754/Active site: Lys #status predicted (Covalent) #status predicted F;754/Active site: Lys #status predicted (Tyr) (covalent) (by protein kinase C) #status predicted F;754/Active site: Lys #status predicted (Tyr) (covalent) (by autophosphorylation) #stat Query Match (A5.3%; Score 3086.5; DB 1; Length 1223; Best Local Similarity 48.4%; Pred. No. 76-119; Matches 628; Conservative 175; Mismatches 149; Indels 145; Gaps 25; Matches 628; Conservative 175; Mismatches 149; Indels 145; Gaps 25;</kin></tmn></tmm></tmm></ee2></ee2></ee1></ext> | 13 RGAAVLVLLLGVALCSAVEEKKVÇGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLE  62 LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD  13 TYVEHNRDLTFLKTIQEVAGYVLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH  122 PLANTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPOLCYQDTILMKDIFHKANQLAL  133 -MNKTQGLRELPWKRLSEILNGGVKISNNPKLCNMDTVLWNDITDTSRK-PL  182 TLID-TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ  183 TVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCHNQ | QY 240 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 299  |

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ectes: Homo sapiens (man)

te: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999

te: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999

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ownan, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; N

Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993

tle: Ligand-specific activation of HER4/pl80erbB4, a fourth member of the epidermal

ference number: A47253; MUID:93189574; PMID:8383326
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A)Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
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                                                                                              9 WGLLLALLPPGAA----STQVCTFNNFTVSFWLRVPKVSASHLE-----LYQGCQVV
                                                                      Gaps
                                                Length 1308;
                                                                      Indels
                                                DB 2;
                                              43.6%; Score 2968.5; DB 2;
45.2%; Pred. No. 4.8e-114;
tive 183; Mismatches 370;
C;Keywords: ATP; growth factor receptor F;716-981/Domain: protein kinase homology <KIN> F;724-732/Region: protein kinase ATP-binding motif
                                                                      Conservative 183;
                                                          Similarity
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protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish
N;Alternate names: epidermal growth factor receptor homolog; kinase-related transformin C;Species: Xiphophorus maculatus (southern platyfish)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C;Accession: S06142; 813809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Robert Nature 34, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu lo A;Reference number: S06142; MUID:90015140; PMID:2797166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; MCCCULE type: DNA
A; Recule type: DNA
A; Residues: 1-1166 <WIT.
A; Residues: 1-1166 <WIT.
A; Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
A; Cross-references: W.; Schartl, M.
Chcogene 6, 73.80, 1991
A; Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophor A; Reference number: S13807; MUID:91125882; PMID:1846957
A; Accession: S13809
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A; Map position: Y
A; Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; tyr
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 1-25/Domain: signal sequence #status predicted (SIG>
F; 707-972/Domain: protein kinase homology <KIN>
F; 707-972/Domain: protein kinase ATP-binding motif
| | | ::|| GHSPPPAYTPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCN 1108
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                                                                                                                                                            GAAKGLOSLPTHDPSPLORYSEDPTVPLPS-----ETDGYVAPLTCSPOPEYVNOPDV
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A;Molecule type: DNA
A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
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seq4-5-25-14.rpr

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| Oy 1232 APPSTFKGTPTAENPEXLG 1250  | RESULT 9 A3623 Kinase-related transforming protein (erk C;Species: Homo sapiens (man) C;Date: 04-0ct-1991 #sequence_revision 1 C;Accession: A36223; 159164 | R;Kraus, M.H.; Issing, W.; Miki, T.; Por<br>Proc. Natl. Acad. Sci. U.S.A. 86, 9193-5<br>A,Title: Isolation and characterization<br>A,Reference number: A36223; WUID:9008323<br>A,Accession: A36223             | A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-1342 < KRA> A.Cross-references: GB:M29366 R.Plowman, G.D.; Whitney, G.S.; Neubauez | Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4<br>A.fritle: Molecular cloning and expressic<br>A.Reference number: I59164; MUID:9031131<br>A.Accession: I59164 | A.Status: preliminary, translated from C<br>A,Molecule type: mRNA<br>A,Residues: 1-559, 'G', 561-957, 'F', 959-10<br>A,Cross-references: GB:M34309: NID:G1833 | C;Genetics: A;Gene: GDB:ERBB3; HER3 A;Cross-references: GDB:119880; OMIM:190 | A, Map Dosition: 14413-14413 C, Superfamily: unassigned Ser/Thr or Tyr C, Keywords: ATP; phosphotransferase C, Keywords: ATP; phosphotransferase F, 7707-921 Domain: protein kinase homolog | Ouery Match 35.3%; Score Best Local Similarity 40.3%; Score Matches 310. Conservative 19.1 Wish | LPPGAASTQVC  | 65 6   | 125  | 123   | Db 176 VKDNGRSCPFCHEVCKG-RCWGPGSE Qy 244 CTGPKHSDCLACLHFNHSGICELHCE    | 235  | Db 295 V-VDQTSCVRACPPDKMEVD-KNGLK  Qy 364 FAGCKKIFGSLAFLPESFDGDPASNI  Db 351 FVNN-RTIGNLAFLIFGLAGDBWRY | 424  |
|---|--|--|--|--|---|--|---|---|--|--|--|---|--|--|--|--|
| 111 YEGNFTLLVMSNYQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVET1 167 168 LMKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-AR 226 | 227 CKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMRNPE 286   | 288 IKYTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVCDGIG 345 347 MEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVPETLEEI 406 346 IGSLSNTIAVNSTNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLWNLTTVKEI 405 | TGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGL<br>          :::        ::      : :   :   | ALIHHNTHLCFVHTVPMDQLFNNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGP :: :     :     :  | 5.26 TQCVNCSQFLRGQECVEERYUQGLPREYVNARHCLPCHPECQPQNGSYTCFGFEADQCV 585  | 586 ACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE 645         | 646 QRASPLTSIVSAVVGILLVVVLGVVFGILIKRROOKIRKYTMRRLLQETELVEPLTPSGA 705<br>  :   | 706 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANK 765<br>                        | 766 EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW 825<br> : | 826 CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP 885 | 886 IKWWALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPP 945 | 946 ICTIDVYMIMVKGWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFY 1005 | 1006 RSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP 1065 | 1066 SEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSET 1124 | 1125 DGYVAPLTCSPQPBYVNQPDVRPQPPSPREGPLP-AARPAGATLERAK 1171<br>   | 1172 TLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERG 1231 |
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er, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G. -4909, 1990
ion of another epidermal growth factor receptor-r 312; PMID:2164210
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                                                             opescu, N.C.; Aaronson, S.A.
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nn of ERBB3, a third member of the ERBB/epidermal
234; PMID:2687875
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rbB3) (EC 2.7.1.-) precursor - human
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I. No. 3.6e-91;
ismatches 447; Indels 146; Gaps
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3990; PIDN:AAA35979.1; PID:g306841
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Cross-references: GB:U29339; NID:g915389; PID:g915390
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                                                                                                                                                                         886 GKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVWV
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                                                                               THONFINGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                               SGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSA
                                                                                                                                                           VVGILLVVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
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                                                                                                                                                                                                                                                                                                 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LPAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEYLTPQGGAAPQP
                       DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                           TKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PLTCSPOPE----YVNOPDVRPOPPSPREGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---QDPPERGAPPSTFKGTPTAENPEYL 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYM 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 1 growth factor receptor homolog precursor - rat NyAlternate names: ErbB3 protein, HER3 protein C)Species: Rattus norvegicus (Norway rat) C)Species: Rattus norvegicus (Norway rat) C;Accession: JC4387  
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G Gene 165, 279-284, 1995  
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the A;Reference number: JC4387; WJD:96096535; PMID:8522190  
A;Reference number: JC4387; WJD:96096535; PMID:8522190  
A;Rocession: JC4387  
A;Rolecule type: mRNA  
A;Residues: (1-1339 cHEL>
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A.Experimental source: liver
A.Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
A.Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
A.Note: The authors translated the codon AAC for receptor that transduces signals to to Genetics:
A.Gene: ErbB3
A.Gene: ErbB3
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolor, Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolor, S.10-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F.60-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F.640-659/Domain: transmembrane #status predicted <TMM>
F.65970/Domain: protein kinase homology <KINN>
F.713-721/Region: protein kinase Arp-binding motif
F.939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr) (**)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::: | : | : | : | : | HOILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLMSKPHLVIAVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVCP-GTLNGLSVTGDADNQYQTL------YKLYEKCEVVMGNLEIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTNRSRACHPCSPMCKGSRCWGBSSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKNNGANCPPCHEVCKG-RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHDECAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPONLOVIRGRILHNGAYS-LTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 EECRVIQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THCNFLQGEPREFVHEAQCFSCHPECLPMEGTSTYNGSGSDACARCAHFRDGPHCVNSCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 1339
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.2%; Score 2327.5; DB 2; Length Best Local Similarity 40.6%; Pred. No. 6.8e-88; Matches 519; Conservative 170; Mismatches 422; Indels
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| NYYLEE 825 Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL | Oy 697 VEPLTPSGAMPNQAQWRILKETELRKVKULGSGAFGTVYKGIWIPDGENVKIPVAIKVIR<br> | 1  | QY         817 LGSQDLIAWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE           :: | 1068 Qy 877 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE | Qy 937 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG | RPQPP 1150         QY         996 PASPLDSTFYRSLLEDDDMGDLVDABEXLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG | -KDVFAFGGAVE 1192 QY 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ | Qy         1111 RYSEDPTVPLPSET DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE | OY 1169 RAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAF | varus protein-tyrosine kinase  Qy 1214 SPAFDNLYYKDQDPPERGAPPSTFKGTPTAENPEYLGLDVP   | L.B.; Raines, M  | processing and pro   |   | 0:g211750<br>as Gallus gal   |   | tyrosine-specific p   | Science 224, 1456-1459, 1984  A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new A;Reference number: A38022; MUID:84223957; PMID:6328658                      | A;ACCEBBION: A38022<br>A;Molecule type: DNA<br>A;Residues: 1-28, W', 30-139, 'F',141-145,'V',147-152 <deb></deb> | A;Cross-references: GB:K02006 | 18; |
|---|---|--|--|--|---|--|---|---|---|--|--|--|---|--|---|---|--|--|-------------------------------|-----|
| HAHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIAKGMYYLEE                | VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRR<br> -      | FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC | WMIDSECRPRERELVSEFSRWARDPQREVVIONEDLGBASPLDSTFYRSLLEDDDWGDLV                             | DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLBPSEE                       | EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ                          | RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPP<br>   | SPREGPLPAARPAGATLERAKTLSP-GKNGVVKDVF  | NPEYLTPOGGAAPQPHPP 1210<br>  : :    <br>EYEYMNRKRRGSP-FRPP 1209             |   | Docenie-Vytosine Kinase (EC 2./.1.112) erbs - avian leukosis virus<br>N;Contains: amino end of grotein; env protein fragment; protein<br>C;Species: avian leukosis virus, AlV<br>C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change ll- | 0643; A00643<br>Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, | activation in ALV-induced erythroblastosis: novel RNA eritation in MID:8528222; PMID:2988784 | 9 | rensingly of the state of the source is designated intry CHKERSBF, release 109.0, the source is designated ein is synthesized as a gag-env-erbB protein. | oenerics:<br>Gene: gag-env-erbB<br>Superfamily: epidermal growth factor receptor; protein kinase homology | phosphotransferase; transforming protein<br>(fragment) #status predicted <gag><br/>n (fragment) #status predicted <env></env></gag> | 60-698/Product: protein-tyrosine kinase erbB #status predicted <erb 194-459="" <kin="" domain:="" homology="" kinase="" protein=""> 202-210/Region: protein kinase ATP-binding motif</erb> | acus predicted<br>25.9%; Score 1766.5; DB 1; Length 698;<br>52.2%; Pred. No. 2.8e-65;                            | (00 00:11                     |     |

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A;Gener: FlyBase:Egfr
A;Grose-references: FlyBase:FBgn0003731
A;Grose-references: FlyBase:FBgn0003731
A;Grose-references: FlyBase:FBgn0003731
A;Grose-references: FlyBase:FBgn0003731
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; glycoprotein; phosphoprotein; c;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; promain: raracellular #status predicted <TMT>
F;73-75-1330/Domain: intracellular #status predicted <INT>
F;808-1072/Domain: protein kinase ATP-binding motif
F;808-1072/Domain: protein kinase ATP-binding motif
F;122,300,324,363,518,688,655,700/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;73-Minding site: phosphate (TMT) (covalent) (by protein kinase C) #status predicted
F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predic
    A;Molecule type: DNA
A;Residues: 'A', 832-866,'V', 868-943,'QTPSLVK' <WAD>
A;Cross-treferences: EMBL:X02293; NID:g7922; PIDN:CAAAS157.1; PID:g929565
C;Comment: This sequence is tentative because the introns have not been identified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 LVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFG 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGLRELQLRSITEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHESCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 RSCPQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH------AGNIDSFRNCTVIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VQGYVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSPMCKGSRCWGESSEDCOSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLAFLPESFDG--DPASNTA-----PLOPEQLQVFETLEETTGYLYISAWPDSLPDLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FONLOVIRGRILHNGAY-SLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AIQXEPEQKVWVNENLRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSVQRGRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 GSWHGSVPYLQELQFQWHLHRRLWLYIQVSINSTQDKSNEHQLTDACYSPSVPTSLTIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 ARYAIQSAGLAMELEQITARSASMRHSKTLPAEGRQVPRWVFLGVCASARAGIAEPLAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----CHOLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV---NARHCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 AVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCETEC----PADHYTDEEQRECFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHPECQPQNGSVTCFGPEADQCVACAHYK-----DPPF-----CVARCPSGVK-PDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 RHPEC---NG---CTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTSKCPLEMRHVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Length 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                 371;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.3%; Score 1652.5; DB 1; Length Best Local Similarity 29.9%; Pred. No. 2.3e-60; Matches 413; Conservative 180; Mismatches 415; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 QLFRNPHQALLHTANRPEDEC----
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N. Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C. Species: Drosophila melanogaster

C. Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999

C. Jacession: A06640; A38021

R. Livrneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.

Cell 40, 599-607, 1985

A. Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding A; Reference number: A00640; MUID:85124611; PMID:2982499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1330 <LIV>
A;Residues: 1-1330 <LIV>
A;Cross-references: EBL:K03054
B;Cross-references: EBL:K03054
B;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature 314, 178-180, 1985
A;Title: A Drosophila genomic sequence with homology to human epidermal growth factor A;Reference number: A38021; MUID:85137938; PMID:2983232
A;Accession: A38021; MUID:85137938; PMID:2983232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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                                           16;
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                                                                                   CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                          RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                           Indels 126;
  Length 604;
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|---|---|
| Query Match Best Local Similarity 54.9%; Pred. No. 1.6e-60; Matches 345; Conservative 70; Mismatches 121; Indels 92; Gaps 15; | Matches 345;         Conservative 69;         Mismatches 122;         Indels 92;         Gaps           578         GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEGACQPCPINCTHSCVDL |
| OY 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKPDEEGACQPCPINCTHSCVDL 637  | Db 1 GPDHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP 57  Qy 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETEL 696  :                                  |

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996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
                                                                                                                                                              1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
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       VEPLTPSGAMPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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Search completed: July 22, 2003, 09:07:53 Job time : 30.9062 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2304 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

SEQ4-5-25-14 6812 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | P04626 homo sapien | P06494 rattus norv | Q60553 mesocricetu | P00533 homo sapien | mus n | Q15303 homo sapien | Q62956 rattus norv | P13388 xiphophorus |            |          |            | P00534 avian leuko |            |            | P13387 gallus gall |            | P70424 mus musculu |            | P06213 homo sapien |            | _         | _          |          | Q25197 hydra atten |           | _         |            | Q60751 mus musculu | P24062 rattus norv |       | m          | 994 | Q07494 gallus gall |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|-------|--------------------|--------------------|--------------------|------------|----------|------------|--------------------|------------|------------|--------------------|------------|--------------------|------------|--------------------|------------|-----------|------------|----------|--------------------|-----------|-----------|------------|--------------------|--------------------|-------|------------|-----|--------------------|
| SUMMARIES | ID                    |                    | ERB2 RAT           | ERB2 MESAU         | EGFR HUMAN         |       | ERB4 HUMAN         | ERB4_RAT           | XMRK_XIPMA         | ERB3 HUMAN | ERB3_RAT | EGFR_DROME |                    | ERBB_AVIER | ERBB AVIEU | EGFR_CHICK         | LT23_CAEEL | ERB2_MOUSE         | ILPR_BRALA | INSR HUMAN         | MIPR_LYMST | IRR_MOUSE | INSR MOUSE | INSR_RAT | HTK7_HYDAT         | IRR_HUMAN | IRR_CAVPO | IG1R HUMAN | IG1R_MOUSE         | IG1R_RAT           |       | INSR_DROME |     | EPB1_CHICK         |
|           | DB                    | п                  | ч                  | -                  | -                  | Н     | -                  | 7                  | 7                  | П          | 7        | Н          | H                  | Н          | -          | Н                  | Н          | Н                  | Н          | Н                  | н          | н         | Н          | -        | н                  | ч         | П         | Н          | н                  | -1                 | -     | Н          | ч   | ~                  |
|           | Query<br>Match Length | 1255               | 1257               | 25                 | 1210               | 1210  | 1308               | 1308               | 1167               | 1342       | 1339     | 1426       | 634                | 604        | 540        | 703                | 1323       | 245                | 1363       | 1382               | 1607       | 1300      | 1372       | 1383     | 1477               | 1297      | 1300      | 1367       | 37                 | 37                 | 33    | 2146       | æ   | α                  |
| do        | Query                 | ω.                 | 9                  |                    | 45.9               | ٠.    | 43.6               | 43.3               | 6                  | S.         | 34.5     |            |                    |            | 23.9       |                    |            | 16.8               |            | 10.3               | 10.3       |           | 10.2       |          | 10.2               |           |           |            | 9.3                | 9.<br>9            | ٠     | 9.1        | ٠   |                    |
|           | Score                 | 9                  | 28                 | 5879.5             | 3130               | 3112  | 2968.5             | 2949               | 2705.5             | 241        | 2350.5   | 1931       | 1749.5             | 1703       | 1630       | 1587               | 1297       | 1142.5             | 724        | 700                | 699.5      | 695       | 694.5      | 694      | 694                | 9         | 684.5     | 645        | 635                | 631.5              | 625.5 | 621.5      | 9   | 591.5              |
|           | Result<br>No.         | 1                  | 7                  | М                  | 4                  | S     | ø                  | 7                  | œ                  | σ          | 10       | 11         | 12                 | 13         | 14         | 15                 | 16         | 17                 | 18         | 19                 | 20         | 21        | 22         | 23       | 24                 | 22        | 56        | 27         | 28                 | 29                 | 30    | 31         | 32  | 33                 |

|                          | P07949 homo sapien<br>P29317 homo sapien<br>P09759 rattus norv |                          |                          |                          |            |
|--------------------------|--|--------------------------|--------------------------|--------------------------|------------|
| EPA2_MOUSE<br>EPB4_MOUSE | RET HUMAN<br>EPAZ HUMAN<br>EPB1 RAT                            | EPBB_XENLA<br>EPB1_HUMAN | EPBA_XENLA<br>FAK1_CHICK | FAK1_XENLA<br>HT16_HYDAT | FAK1_MOUSE |
|                          | ннн  | ਜ ਜ                      |                          |                          | 7          |
| 977                      | 1114<br>976<br>984   | 902<br>984               | 985<br>1053              | 1068                     | 1052       |
| 8.7                      | 0 8 8<br>0 6 6   | 8 8<br>5.5               | 80 80<br>7. 4.           | 8 8<br>4 6               | 8.3        |
| 589.5<br>588             | 588<br>584.5<br>583.5  | 579<br>577.5             | 576.5<br>573.5           | 569<br>567               | 563        |
| 3.4<br>3.5               | 36<br>37<br>38   | 39                       | 41                       | 4 4<br>4 4               | 45         |

## ALIGNMENTS

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AVVGILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILK
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Pred. No. 0;
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137909 MW; 39E9DFDA04DCF962 CRC64;
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.072, ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.012.
ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
TRANSMEMBRANE; PSS0011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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PROTEIN KINASE.
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InterPro; IPR001719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; Yrp_motif.
Pfam; PF00069; pkinase; I.
Pfam; PF00130; Rutin-like; I.
Pfam; PF0130; Recep L.domain; 2.
Pfam; PF02757; Yrp; Z.
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EMBL; M11761; AAA35808.1; JOINED.
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11766; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; JOINED.
EMBL; M11730; AAA35898.1; ---
EMBL; M12036; AAA35978.1; ---
EMBL; X03363; CAA27060.1; ---
EMBL; X034571; A24571.
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Genew; HGNC:3430; ERBB2
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HSSP; P11362; 1FGK
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PEYVNOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY 1196
                                                                                                                                                                                                                                                                        KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD 1016
                                                                                                                                                                                                                                                                                                                                        LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076
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                                                                                                                                                                                                         RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV 956
                            RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV
           ETELEKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANKET LDEAYVMAG
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                                                                           VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL
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MEDLINE=86118662; PubMed=3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN'1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 37, Last sequence update)
Receptor protein-ty.nosine kinase erbs-2 precursor (EC 2.7.1.112)
(p185srb82) (NEU proto-oncogene) (C-erbs-2) (Epidermal growth factor receptor-related protein).
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MEDLINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in the vertebrate nervous system.", Neuron 6:691-704(1991).
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MEDLINE=91222560; PubMed=2025425;
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                                                       YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI
                                                                                             LRRRFTHQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPPICTIDVYMI
                                                                                                                                                 MVKCWMIDSECRPREVELVSEFSRMARDPQREVVIQNEDLGPASPLDSTFYRSLLEDDDM
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                                                                                                                                                                                                                                                                                                                            Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-SEPPED (NEU proto-oncogene) (C-erbB-2)
ERBBZ OR NEU.
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N-SINKED (GLONAC. .) (POTENITAL).
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PROTEIN KINASE

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Pfam; PP01030; Recept L. domain; 2.
Probom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM0019; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Prosine-received Receptor; Signal;
Procedum Receptor; Signal;
Proto-oncogene; Disease mutation.
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86.2%; Pred. No. 4.8e-306;
live 60; Mismatches 105;
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                                                                                                                         InterPro; IPPR000494; EGFR L domain.
InterPro; IPR000719; Euk phinase.
InterPro; IPR001214; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00065; pkinase; I
                                                                                              EMBL; D16295; BAA03801.1; -.
HSSP; P11362; 1FGK.
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Matches 1085; Conserv
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Gaps

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KCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD 1016 476 476 TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV 356 VARCPSGVK)DLSYMPIWKYPDEEGMCQPCPINCTHSCVDLDERGCPAEQRASPATSIIA MELAALCRWGLILALLPPGAASTQVCTFNNFTVSFWLRVPKVSASHLE----LYQGCQVV MELAAWCGWGLLLALLSPGASGTQVCTGTDMK----LRLPASPETHLDIVRHLYQGCQVV QGNLELTYI.PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAV LDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKN NQLALTLIUTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCC HEQCAAGCT'GPKHSDCLACLHFNHSGI CELHCPALVTYNTDTFESMPNPEGRYTFGASCV HEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV TSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWP TSANIQEFAGCKKIFGSLAFLPESFDGNPSSGIAPLTPEQLOVFETLEEITGYLYISAWP DSLPDLSVPQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVWAG EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWIALESILR VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS ETELRKVKVI,GSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAG VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLA 1017

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1196
           PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ 1136
                                                                                             LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                       Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells."; Nature 309:418-425(1984).
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MEDLINE=21100872; PubMed=11161793;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
                                             PEYVNOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
                                                                                                                                                      EGFR HUMAN STANDARD; PRT; 1210 AA. P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732; O00658; Q9B228; Q9B2X1; Q9H3C9; Q9UMD9; Q9UMG5; Q92795; O00732; Q1-UU-1986 (Rel. 01, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (RC 2.7.1.112) (Receptor protein-tyrosine kinase ErbB-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative genomic sequence analysis and isolation of human and mouse alternative EGFR transcripts encoding truncated receptor isoforms.";
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97256547; PubMed=9103388; Ilekis J.V., Gariti J., Niederberger C., Scoccia B.; Expression of a truncated epidermal growth factor receptor-like protein (TEGFR) in ovarian cancer."; Gynecol. Oncol. 65:36-41(1997).
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Reiter J.L., Maihle N.J.;
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MEDLINE=95382957; PubMed=7654368;
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MEDLINE-85270438; PubMed=2991899; Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.; "Characterization and sequence of the promoter region of the human epidermal growth factor receptor gene."; Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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Mroczkowski B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
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MEDLINE=81196372; PubMed=6326261;
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Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
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Biochem. Biophys. Res. Commun. 124:125-132(1984).
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MEDLINE=84245835; PubMed=6330563;
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                                                                                                                                                       extracellular domain of the receptor.";
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Submitted (SEP-1997) to the SWISS-PROT data bank
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Nature 309:270-273(1984).
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Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                           ASN-528.
MEDLINE-96398132; PubMed=8962717;
Smith K.D., Davies M.J., Balley D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster
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receptor and HER2/neu are located in their carboxyl-terminal tails.
Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
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SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                             ASN-444
                                                                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568
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TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is
                                                                                                       CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413;
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MEDLINE=20198209; Pubmed=10731668;
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STOVCTFNNFTVSFWLRVPKVSASHLELYQGCQVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSNMSMDFGNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCC
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SPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET---DGYVAP 1130
                                                                                VENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----PERGAP 1233
                                                                                              1133 VGNPEYLNTVQ-----PTCVNSTPDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKP 1183
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
FEXPESSION Of the epidermal growth factor receptor gene is regulated in mouse blastocyste duting delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                  1032 TPLLSSLSATSN--NSTVACIDRNGLOSCPIKEDSFLORYSSDPTGALTEDSIDDTFL--
                                        1131 LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The mouse waved-2 phenotype results from a point mutation in the EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain, MEDIATE=912866; PubMed=2030916; MEDIATE=912866; PubMed=2030916; Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.; "Comparison of EGF receptor sequences as a guide to study the ligand binding site.";
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
STRAIN=B6/T0986, PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
Avid A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
                                                                                                                                                                                                      001279.
001279.
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H;
Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Liver;
Hibbs M.L.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 PRT; 1210 AA
                                                                                                                         1234 PSTFKGTPTAENPEYL 1249
                                                                                                                                             1184 NGIFKGS-TAENAEYL 1198
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SEQUENCE OF 969-1117 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor tyrosine kinase.";
Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-714 FROM N.A.
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FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF, AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HERRIN-BINDING EGF, GP30 AND VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                               cell DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R MGD; WGI195294; EGFR L domain.
R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000494; EGFR L domain.
InterPro; IPR00179; Eux Difinase.
R InterPro; IPR001245; Tyr Dkinase.
R InterPro; IPR001245; Tyr Dkinase.
R Eam; PF00169; Pkinase; I.
R Pfam; PF00170; Furin-like, 1.
R Pfam; PF00170; Eux Diffinase; I.
R SWART; SW00261; FU; J.
R SWART; SW00261; FU; J.
R SWART; SW00109; PROTEIN KINASE_ATP; 1.
R PROSITE; PS00110; PROTEIN KINASE_ATP; 1.
R PROSITE; PS00110; PROTEIN KINASE_DOM; 1.
R PROSITE; PS00110; PROTEIN KINASE_DOM; 1.
R TAAISMEMDYANE; GlycoproteIn; Receptor; Signal; Transferase;
T SIGNAL
                                                                     tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANBOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
EPIDERMAL GROWTH FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X59698, CAA42219.1; -. EEMBL, 106864; AAA33029.1; -. EEMBL, Z15608; CAA78249.1; -. HSSP, P11362; 1FGK.
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|  | RESULT 6  ERB4 HUMAN  LD ERB4 HUMAN  AC 015303,  AC 015303,  DT 15-DEC-1998 (Rel. 37, Created)  DT 15-DEC-1998 (Rel. 37, Last sequence update)  DT 15-DEC-1998 (Rel. 37, Last sequence update)  DT 15-DEC-1998 (Rel. 41, Last annotation update)  DT 15-DEC-1998 (Rel. 41, Last annotation update)  DT 15-DEC-1998 (Rel. 41, Last annotation update)  DE Receptor protein-tyrosine kinase erbB-4 precursor (BC 2.7.1.112)  DE REBB4 OR HER4.  CO EMARAPOLAS Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;  CO Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.  CO Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.  CO Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.  RN 12SUBERE RESEAS Cararrioma;  RN FEDLINE-93189574; PubMed-8383326;  RN FO L., Weubauer M.G., Shoyab M.;  RN FOLINE-91996-11 activation of HER4/pl80erbB4, a fourth member of the RT epidermal growth factor receptor family."; RN EDLINE-97476-287; PubMed-9334263;  RN FEDLINE-97476-287; PubMed-9334263;  RN MEDLINE-97476-287; PubMed-9334263;  RN MEDLINE-97476-287; PubMed-9334263;  RN RELINE-97476-287; PubMed-9334263;  RN RIBBILNE-97476-287; PubMed-97476-1750, RN RIBBILNE-97476-1750, RN RIBBIL |
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BY SIMILARITY.
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                                                                                                                                                                            C -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE RECEPTORS (POTENTIAL).

C -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE RECEPTORS (POTENTIAL).

C -1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; JM-A (SHOWN HERE) AND JM-B;

C -1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; JM-A (SHOWN HERE) AND JM-B;

C -1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; JM-A (SHOWN HERE) AND JM-B;

C -1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; JM-A (SHOWN HERE) AND JM-B;

C C -1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; JM-A (SHOWN HERE) AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOPORMS ARE EXPRESSED IN CRREBELLUM, BUT ONLY THE JM-B ISOPORM IS EXPRESSED IN THE HEART.

C -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,

C -1- TISSUE SPECIFICITY: EXPRESSED AND BREAST. LOWER LEVELS IN THYMUS,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION OF SELECTAL MUSCLE, PARATHYROID, CEREBELLUM,

C -1- TISSUE SPECIFICATION ON TYROSINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                       phorbol ester.";
J. Biol. Chem. 272:26761-26768(1997).

-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG--
2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
  novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF02757; YLP; 2.
Pr0000n; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 4; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                   tissue distribution and differential processing in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L07868; AAB59446.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:3432; ERBB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase;
Pfam; PF00757; Furin-lik
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|   | 30,  | 23   | 116  | 176  | 235  | 295<br>289  | 355  | 415   | 475  | 535   |
|---|--|--|--|--|--|---|--|---|--|---|
| BY SIMILARITY BY  | Pred. No. 6.7e-151<br>183; Mismatches 370<br>STQVCTFNNFTVSFWLRVPKV | WVWVSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVV | QGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAV<br> | LDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKN<br> | NQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGG-ARCKGPLPTDC | CHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASC<br>   :      :      :      : | VTACPYNYLSTDVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRA<br> | VTSANIQBFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLXISAM<br>   :    : | LSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLC<br> | VHIVPWDOLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQFL |
| , ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;   |  | AAGTVQPSD  | LPTNASLSF<br>:      <br>!EHNRDLSF                                | INTTPVTGAS<br> <br>INF   | DINRSRACH  | CTGPKHSDC<br> :    :  <br>CSGPKDTDC   | TSTDVGSCT  | FAGCKKIFG<br>       <br>FINCTKING   | DSLPDLSVFQNLQVIRGRI<br>::       <br>PNMTDFSVFSNLVTIGGRV    | OLFRNPHOA   |
| 11110000000000000000000000000000000000  | milari<br>Cons<br>GLLLAL   | WVWVSLLV   | DGNLELTY<br>    : <br>MGNLEITS                                   | LDNGDPLNNT<br> <br> -<br>FLNYRKDGNF                              | NQLALTLIDTNRS<br>   :   <br>WPSNLTLVSTNGS                    | CHEQCAAC  | VTACPYNYL<br>    : ::<br>VKKCPHNFV                               | VTSANIQE  | PDSLPDLS<br>  ::    <br>PPNMTDFS                           | FVHTVPWI<br>:   :   |
| ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID<br>ULFID | SO   |  | 57 (   | 117 1  | 1771   | 236 (   | 296 7  | 356   | 416 1  | 476   |
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR001019; Euk pkinase.
InterPro; IPR001014; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF001099; TYRKINASE.
                                                                                                                                                  Biol. Chem. 273:10261-10269(1998)
                                                                                                                                                                                                   TISSUE-Sciatic nerve;
MEDLINE-91222560; PubMed=2025425;
                                      MEDLINE=98221155; PubMed=9553078;
                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1031-1198 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF041838; AAD08899.1; -.
EMBL; US2531; AAC53051.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                  SEQUENCE OF 848-901 FROM N.A.
   SEQUENCE FROM N.A.
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   TAKA BERKARAKAN BERKARAKAN BERKARAKAN BERKARAK BER
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                                                                                                                               588 NCVEKCPDGLQGANSF--IFKYADPDRECHPCHPNCTQGCNGPTSHDC1YYPWTGHSTLP
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                                                         644 AEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
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                                                                                                        FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC-
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15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor
ERBB4 OR TYRO-2.
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15-DEC-1998 (Rel. 37, Created)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Droinformatics Institute or the European of the Swisser Sw
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SUBUNIT: HONDOIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE SUBUNIT: HONDOIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE SUBCELLULAR LOCANITAL).
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
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SMART; SM00261; FU; 4.
SMART; SM00261; TU; 4.
SMART; SM00219; TYRC; 1.
PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Iransferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation. SIGNAL
                                                                                                                                                                      "Neuregulins promote survival and growth of cardiac myocytes. Persistence of Erbi2 and ErbB4 expression in neonatal and adult ventricular myocytes.";
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Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J.,
Marchionni M.A., Kelly R.A.;
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Neuron 6:691-704(1991).
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|   | y 289 YTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGME 348   :           :     | 349 HLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFFTLEEITG | 341 SLMSAQTVDSSNIDKFINCTKINGNLIFLVTGIHGDPYNAIDAIDPEKLNVFRTVREITG | 409 YLYISAMPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALI | 401 FLNIQTWFPNMTDFSVFSNLVTIGGRVLVSGLSLLILKQQGTISLQFQSLKEISAGNITI | 469 HHNTHLCEVHYVPMDQLFRNHQALLHTANKPEDECVGEGLACHQLCARGHCWGPGTQC 528 | 524 VNCSOFT RECREVERENT OFF. PREVVNR PHCI. PCHPECOP. ONGSVTCFGBBADOCVAC | 521 LSCRRFSRGKICIBSCNLYDGEFRBFENGSICVECDSQCEKWEDGLLTCHGPGPDNCTKC | 588   | 581 SHFKDGPNCVEKCPDVLQGANSFIFKYADQDRECHPNCTQGCNGPTSHDCIYYPW 638 | 643      | 639            | 696 LVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVL | 694 LVEPLTPSGTAPNQAQLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETVKIPVAIKIL | 756 RENTSPRANKEILDEAYVMAGYGSPYSKLLGICLTSYVQLYYQLMPYGCLLDHYRENRG #15<br>  | 816 RLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDET | 814 NIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEK 873                             | 876 EXHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLL 935   -   - | 936 FKGEBIEDDDDTGTTDVVMTMVKCMMTDSECPBBRBBIJSBESRMABDDDSPRVVIONED-1. | 934 EKGERLPOPPICTIDVYIVMVKCWMIDADSRPKFKELAAEFSRWARDPORYLVIQGDDRM 993          | y 995 GPASPLDSTFYRSLLEDDDMGDLVDABEYLVPQQGFFCPDP | 1036APGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVPDGDLG 1091 | 1092 MGAAKGLOSLPTHDPSPLQRXSEDPTVPLPSETDGVVAPLTCSPQPEVVNQPD | :  | y 1145 VRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAA 1204 | 1205 PQPHPPPA       | 1195PPKAEDEYVNEPLYLNTFTNALGNAEYMKNSLLSV                           | y 1231 GAPPSTFKGTFT   |   |
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| • | RECEPTOR PROTEIN-TYROSINE KINASE ERBS-4. EXTRACELLULAR (POTENTIAL). POTENTIAL. COMPANYIAL. | CYS-RICH.<br>CYS-RICH.   | PROTEIN KINASE.<br>ATP (BY SIMILARITY)                           | ATP  | BY   |  | BY  | BY   | BY SIMILARITY.  BY SIMILARITY.  DO BY CIMILARITY. | BA  | BY       | BY<br>BY<br>BY | BY<br>BY   | BY SIMILARITY. PHOSPHORYLATION (AUTO-) (BY SIMILAR               | B PHOSPHORYLATION (AUTO-) (BY SIMILARITY). B PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 4 PHOSPHORYLATION (AUTO-) (BY SIMILARITY). | N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).    | 3 N-LINKED (GLCNAC) (POTENTIAL). 8 N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). | N-LINKED (GLCNAC ) ( N-LINKED (GLCNAC ) ( N-LINKED (GLCNAC ) (               | N-LINKED (GLCNAC) (N-LINKED (GLCNAC)                                | S -> N (IN REF. 3)<br>PYT -> SYR (IN REF. 3)<br>16957 MW; D944BB0996A08B41 CR | 38; Scor<br>08; Pred<br>190: N                  | -ALLEPGAASTQVCTFNNFTVSFWLRVPKVSASHLEL 4                           | MKLATGLWVWGSLLVAARTVQPSASQSVCAGTENKLSSLSDLEQQYRALRKY 52    | YOGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFE 109  :  - |  | 16                  | KULFHKNNQLALTILLDINRSRACHPCSPMCKGSRCWGESSEDCOSLIRIYCAGGC-ARCK 228 | GPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNFGR 288 |   |
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563; Conservative 156; Mismatches 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schartl M., Schartl M., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSOOLD; PROTEIN KINASE ATP; 1.
PROSITE; PSOOLD9; PROTEIN KINASE TYR; 1.
PROSITE; PSSOOL19; PROTEIN KINASE TOM; 1.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                      Xiphophorus maculatus (Southern platyfish).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopierygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poecillidae; Xiphophorus.
                                                                                           01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=90015140; PubMed=2797166;

Mittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,

Telling A., Robertson S.M., Schartl M.;

"Novel putative receptor tyrosine kinase encoded by the melanoma-
inducing Tu locus in Xiphophorus.";

Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                     1167 AA
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InterPro; IPR001245; Tyr pkinase.
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HSSP; P11362; 1FGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000119; Euk pkinase.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Pfam; PF00069; pkinase; 1. |
| Pfam; PF00757; Furin-like; 1. |
| Pfam; PF00757; Furin-like; 1. |
| Pfam; PF001030; Recep L domain; 2. |
| PRNTS; PR00109; TYRKINASE. |
| ProDom; PD000001; Euk_pkinase; 1. |
| SMART; SM00261; FU; 5. |
| SMART; SM00219; TYRK; 1. |
| SMART; SM00219; TYRK; 1. |
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                                                     STANDARD;
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P13388;
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(POTENTIAL)

(POTENTIAL)

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946 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFY 1005
                                                                                                                                                                                                                                                                             1006 RSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP 1065
                                                                                                                                                                                                                                                                                                                                                                                                                       1104 YLNTNQNSL---PLVSSGSMDDPDY---QAG------YQAAF-----LPQTG 1138
                                                                                                                                                                                                                                                                                                                    1066 SEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSET, 1124
                                                                                                                                                                                                                                                                                                                                       ------PVRENSITLRNISDPTONALEKDL 1053
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                                                                                                                                                                                                                                                                                                                                                                               1054 DGH------EYVNQPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPE 1103
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                                                                       106 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
579 KSAHFQDGPQCIPRCPHGILGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSGCRGD
                                                                                                                                                      CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                                                                                                                                                                        993 SRLLSSDD--DVVDADEYLLPYKRI--------NRQGS------
                              QRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                         EILDEAYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbb-3 precursor (EC 2.7.1.112)
(c-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90083234; PubMed=2687875; Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A. Isolation and characterization of ERBB3, a third member of ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors.", Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1232 APPSTFKGTPTAENPEYLG 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90311312; PubMed=2164210;
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Homo sapiens (Human)
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EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
3.J., Shoyab M.;
                          Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth factor receptor-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Alternative splicing.
                                                                                                                                                                              TISSUE=Placenta;
MEDLINE=9328282; PubMed=7685162;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor tyrosine kinase.";
Biochem. Blopbys. Res. Commun. 192:1189-1197(1993).
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEURECULINS AND NTAK.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000494; EGFR L domain.
InterPro; IPR00719; Euk DkInase.
InterPro; IPR002145; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; Dkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00750; Furin-like; 1.
Probom; PD000001; Euk Dkinase; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
SMART; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00107; PROTEIN KINASE TYR; FALSE NEG.
PROSITE; PS00101; PROTEIN KINASE TYR; FALSE NEG.
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                                                                                                                                                           SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24309; AAA35790.1; -. EMBL; M34309; AAA35979.1; -. EMBL; S61953; AAB26935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:3431; ERBB3.
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HSSP; P11362; 1FGK.
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| FID   216   218   BY SIMILARITY.   | VGAYS-LTLQGLGI.<br>  :    ::   :<br>  RGFSLLIMKNLNV                  |
| 210 218 224 225 224 225 226 229 301 302 301 305 301 301 301 301 301 301 301 301 301 301  | /IRGRILH<br>         : <br> IGGRSLY                                  |
| 110   210   214   110   2214   110   2214   110   2217   120   2217   |  |
| FT DISULETD FT CARBOHYD FT CAR | 424  |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDICING PROTEINS.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00109; TYRKINASE.
Probom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 5.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
TRANSMEMBARA.
TYANSMEMBARA.
TYANSMEMBARA
                                                                                                                                                                                                                                                                                    SEQUENCE OF 922-1097 FROM N.A.
STRAIN-Sprague-Dawley, TISSUE-Sciatic nerve;
MEDLINE-97184212; PubMed-9030624;
MEDLINE-97184412; PubMed-9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";
D. Neurosci. 17:1642-1659(1997).
--- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
--- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
--- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=96096535; PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
Hellyer D.G., Frim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein."
                                                                                                                                                                                       REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
BY SIMILARITY.
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EMBL; U52530; AAC53050.1; --
HSSP; P11362; 1FGR.
INTEPTO; IPR000494; EGFR L. domain.
INTERPTO; IPR000119; EUK DKINASE.
INTERPTO; IPR00124; FUTIN-like.
INTERPTO; IPR001245; TYT DKINASE.
PEam; PF00169; DKINASE; I.
PEam; PF001050; Recep L. domain; 2.
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| 144447777   | h<br>Simila<br>22; Cc   | ALCRV<br> : <br>AVCP-  | LPTN/<br> -<br>TGHN/  | NTTPN<br> <br>YNT  | DTNRS<br>VKNNC   | CTGP!<br> -: <br> CSGP(  | LSTD'<br>:  <br>V-VD(   | FAGC:  | VFONI<br>  | DOLFI<br>:-<br>TRLLI   | EECR!      | THCNI  |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular analysis of the Drosophila EGF receptor homolog reveals that several genetically defined classes of alleles cluster in subdomains of the receptor protein."; Genetics 137:511-550(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II). MEDLINE=94350209; PubMed=8070664; Clifford R., Schupbach T.;
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RADAIN GOOTE C. Garter S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Button G.G., Wortnen J.R., Yandell M.D., Zhang O., Chen L.X.,

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RADAIL J.F., Agbayari A., An H.-J., Andrews-Fennancoh C.R., Miklos G.L.G.,

RADAIL J.F., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,

RADORON R., Benos P.V., Berman B.P., Brotater P., Chandra I.,

RADORON R., Doub L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

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RADAIN R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RADAIN R.J., Brons P.W., Howland T.J., Wei M.-H., Ibegwam C.,

RADAIN M., L.HATVAD D., Howland T.J., Wei M.-H., Ibegwam C.,

RADAIL M., Hauston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Alali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.M., Ketchum R.A.

RADAIN R. Moy M., Murphy B., Mixon W., Mcheod M.P., Mcherson D.,

RADAIN M., Ralush R., McInteen T.C., Morris J., Woshrefi A.,

Radazolo M., Pittenan G.S., Pan S., Pollax J., Pari V., Shan H.,

Radazolo M., Pittenan G.S., Pan S., Pollax J., Wang X.,

Radazolo M., Pittenan G.S., Pan S., Pollax J., Wang X.,

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Radazolo M., Pittenan G.S., Pan S., Pollax J., Wang X.,

Radazolo M., Ritenan G.S., Pan S., Pollax J., Wang X.,

Radazolo M., Pittenan G.S., Pan S., Pollax J., Pari V., Sheng L.,

Radazolo M., Ritenan G.S., Radanese R.D.C., Scheeler F., Shen H.,

Radibe R., Renington K., Saunders R.D.C., Scheeler F., Shen H.,

Radibe R., Rohnes B.W., Rubin G.M., Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
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MEDLINE=88137988; PubMed=2983232;
WAGAWORTH S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; PubMed=3093080;
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Cell 46:1091-1101(1986).
                                          databases
Clifford R., Schupbach T.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ
                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
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MEDLINE=99102120; PubMed=9882502;
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                                                                                                                                                                                                                                                                                                                                                              Cell 40:599-607(1985).
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332 KEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSCPQDKMDKGG 390
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                                                                            PIYER PRODUCTS: BEFR. L. domain.

R. InterPro: IPR000131; EGFR. L. domain.

R. InterPro: IPR000139; EUK_DKInase.

R. InterPro: IPR001245; Furin-like.

R. InterPro: IPR001245; Tyr_Dkinase.

R. InterPro: IPR001245; Tyr_Dkinase.

R. Pfam; PF00105; Furin-like; I.

R. Pfam; PF00105; Furin-like; I.

R. PROJOS: Recep_L. domain; 2.

R. ProDom; PR00109; TYRINASE.

R. PRODOM; PR00109; TYRINASE.

R. PROSTIE; PR00109; PROTEIN KINASE ATP; I.

R. PROSTIE; PS00107; PROTEIN KINASE TYR; I.

R. PROSTIE; PS00109; PROTEIN KINASE_DOM; I.

R. PROSTIE; PS00119; ROTEIN KINASE_DOM; I.

R. PROSTIE; PS00119; ROTEIN KINASE_DOM; I.

R. PROSTIE; PS00119; PROTEIN KINASE_DOM; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSVPSNKEHHYRNLRDRYTNCTYVDGNLKLTWLPNENLDLSFLDNIREVTGYILISHVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROVPLORLRIVEGTOLF ---- EDNYALAVLDNGDPLNNTTPVTGASPGGLRELOLRSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSEDCOSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 TANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 180; Mismatches 429; Indels 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1931; DB 1; Length 1426;
Pred. No. 1.4e-95;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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SIGNAL 1
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                                                         HSSP; P11362; 1FGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464;
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Best Local S:
Matches 464
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TRANSMEM
DOMAIN
DOMAIN
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ACT SITE
MOD_RES
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EMBL; AF052754; AAC08536.1; JOINED.

EMBL; AF052754; AAC08536.1; JOINED.

EMBL; AF052754; AAC08536.1; JOINED.

EMBL; AF052754; AAC08536.1; JOINED.

EMBL; K03418; AAA51460.1; JOINED.

EMBL; K03418; AAA51460.1; JOINED.

EMBL; K03418; AAA51461.1; JOINED.

EMBL; AF109078; AAD56132.1; JOINED.

EMBL; AF109078; AAD56132.1; JOINED.

EMBL; AF109078; AAD56132.1; JOINED.

EMBL; AF109078; AAD56131.1; JOINED.

EMBL; AF109084; AAD56131.1; JOINED.

EMBL; AF109089; AAD56131.1; JOINED.

EMBL; AF108089; AAD56
                                                                                                                                                                                                                                                                                                                                               Perrimon N., Perkins L.A.;

There must be 50 ways to rule the signal: the case of the Drosophila grants be 50 ways to rule the signal: the case of the Drosophila are ceptor.";

Cell 89:13-16(1997).

-!- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY: INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.

CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE III; ARE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HICHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                         MUTATION
                                                                                                                                                                            Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                         SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND
                                                                                                                                                                                                                                                                                                  [9]
REVIEW.
MEDLINE=97248481; PubMed=9094709;
                                                                                                                                               MEDLINE=92038942; PubMed=1936959;
growth factor receptor.";
Nature 314:178-180(1985).
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---<u>:</u>

42;

Gaps

271

264

437 436 497 557

601

558 NENLRADLCEKNGTICSDQCNEDGCWGAGTDQCLTCKNFNFNGTCIADCGYISNAYK--F 556 NARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP-------

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   706 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMQIAKGMSY:EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                                         MISCELLANBOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS.
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
C-ERB GENE, WHICH LEADS TO C-ERB ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                               CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                          MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A00643; TVCHLV.

R HSSP, P11362; ITCHLV.

R HSSP, P11362; TVCHLV.

R INTERPORT: IPRO01245; TYL Dkinase.

R INTERPORT: IPRO01245; TYL Dkinase.

R INTERPORT: PRO0109; TYRKINASE.

R PFODOM; PD000001; EUK pkinase; 1.

R PROSITE; PS00107; FROTEIN KINASE ATP; 1.

R PROSITE; PS00109; FROTEIN KINASE DOM; 1.

R PROSITE; PS00119; FROTEIN KINASE DOM; 1.

R PROSITE; PS0011; FROTEIN KINASE DOM; 1.

R PROSITE; PS0011; FROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 634;
                MEDLINE=8522822; PubMed=2988784; Nisen T.W., Maronby P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.; "c-erbB activation in ALV-induced erythroblastosis: novel approcessing and promoter insertion result in expression of amino-truncated EGF receptor."; cell 41:719-726 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1749.5; DB 1; Length
; Pred. No. 2.7e-86;
79; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E705E33A0BE01FCC CRC64;
                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M10066; AAA48763.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.33
Matches 370; Conservative
                                                                                                                                               tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 AA;
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138
165
257
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DOMAIN 13
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVIONEDLG--PASPLDSTFYRSLLEDD---DMGDLVDAEEYLVPQQGFFCPDPAPGAGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 MVHHRHRSSSTRSGGGDLTLGLEPSEEEAP-----RSPLAPSEGAGSDVFDG---DLGM 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSP 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1153 REGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL----TPQGGAAPQPH 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | : | : | : | 329 NQNNWAAVGVAAGYM------DLIGVPVSVDNPEYLLINAQTLGVESPIPT 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986
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21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
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                                                                                                                                                                           ----SC-----SKG-----SC----
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InterPro; IPR001245; Tyr pkinase.
Pfam, PP00069; pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-profein kinase; ATP-binding; Oncogene;
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S -> F (IN REF 2).
I -> V (IN REF. 2).
76EBCDD06745D609 CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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52.2%; Pred. No. 7.6e-84;
iive 76; Mismatches 128;
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                             EMBL; K01216; AAA42400.1;
PIR; A00644; TVYUH.
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                                                                                                                                                                                                                           1005 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
                                                                                                                                                                                                                                                                                                                                                          1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS IN CHICKENS.
ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                                                 NGVVKDVP------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima K., "The erbB gene of avian erythroblastosis virus is a member of the src
                                                                                                                                                                                                                                                                                                 ------NSPST-----
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MEDLINE=84223957; PubMed=6328658;
Debuire B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals when type of oncogene.";
Science 224:1456-1459(1984).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian erythroblastosis virus (strain ES4).
Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR FOR EPIDERMAL GROWTH FACTOR. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyrosine-protein kinase transforming protein erbB V-ERBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 FLEESIDDGFL-----PAPEYVNQ--LMPKKPS----
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Last annotation update)
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MEDLINE-84026539; PubMed=6313229;
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15-JUN-2002
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Indels 126;

Length 604;

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                                                                                                                                                                                                                                                                                                                 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
                                                                                                                                                       178 EILDEAYVMASVUNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW 237
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MEDLINE-88261272; PubMed=3260329;
MEDLINE-88261272; PubMed=3260329;
Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M.,
Ullrich A., Vennstrom B., Schlessinger J., Givol D.;
"Chicken epidermal growth factor (EGF) receptor: cDNA cloning,
expression in mouse cells, and differential binding of EGF and
transforming growth factor alpha.";
Mol. Cell. Biol. 8:1970-1978(1988).
-! FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH PACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell bna synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                  - PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISKLPIDSRYQN
                                            CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                  IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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1-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112)
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SUBCELLULAR LOCATION: Type I membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
As single amino acid substitution in v-exbB confers a thermolabile
phenotype to tal67 avian erythroblastosis virus-transformed erythroid
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                                                                                                                                                                                                                                           Avian erythroblastosis virus (strain ts167).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=103898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells.";
Mol. Cell, Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
tyrosine phosphate.
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H -> D (IN THERMOLABILE V-ERBB).
5B53297AA068B65D CRC64;
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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69; Mismatches 119; Indels
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Pred. No. 5.2e-80;
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Last annotation update)
SSPYWIOSGNHO-----INLDNPDY
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ProDom; PD000001; Euk pkinase; 1.
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Best Local Similarity
Matches 341; Conserv
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DOMAIN 1
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15-JUN-2002
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. .) (POTENTIAL)
                              EMBL; M20386; AAA48760.1; -.

R InterPro; IPR000494; EGFR L domain.

InterPro; IPR000419; EUK pkInase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Ffam; PF00137; Furin-like; 1.

R Ffam; PF00130; Recep L domain; 2.

SWART; SM00261; FU; 4.

R PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.

R PROSITE; PS00107; PROTEIN KINASE TYR; PARTIAL.

R PROSITE; PS00109; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS0011; PROTEIN KINASE DOM; PARTIAL.

R PROSITE; PS0011; PROTEIN KINASE DOM; PARTIAL.

R TRANSMEMDYANG; Glycoprotein, Rinase; ATP-binding; Phosphorylation.

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send an email to license@isb-sib.ch)
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Search completed: July 22, 2003, 08:43:53 Job time: 20.2304 secs

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|           | Description                   | O18735 canis famil | Q9qx70 rattus norv | Q9ep98 mus musculu | Q9yh40 xiphophorus | O9w6f6 qallus qall | P79754 fugu rubrip | Q9bih9 anopheles g                            | Q9uk79 homo sapien | OBr2x1 mus musculu | Q86712 avian rous- | Q86714 avian rous- | Q8wyv0 homo sapien | Q64895 avian eryth | Q85468 avian eryth | Q9wvf5 mus musculu | Ogerv6 mus musculu |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | 11<br>11                      | 018735             | 09QX70             | Q9EP98             | Q9YH40             | Q9W6F6             | P79754             | бытне быт | Q9UK79 ·           | Q8R2X1             | 086712             | Q86714             | QBWYVO             | Q64895             | Q85468             | Q9WVF5             | OPERV6             |
|           | DB                            | 9                  | 1                  | 11                 | 13                 | 13                 | 13                 | 2   | 4                  | 11                 | 15                 | 15                 | 4                  | 15                 | 15                 | 11                 | 1                  |
|           | &<br>Query<br>Match Length DB | 1259               | 1209               | 1210               | 1165               | 1137               | 1328               | 1433  | 419                | 367                | 729                | 567                | 412                | 962                | 545                | 655                | 643                |
| d         | Query<br>Match                | 90.8               | 46.1               | 45.6               | 40.2               | 40.1               | 33.6               | 29.4  | 25.9               | 25.5               | 25.2               | 25.2               | 24.9               | 24.3               | 24.1               | 22.0               | 21.8               |
|           | Score                         | 6183               | 3140               | 3109               | 2739               | 2729.5             | 2292               | 2000.5  | 1762.5             | 1739               | 1720               | 1718               | 1697.5             | 1653.5             | 1645               | 1500.5             | 1484.5             |
|           | Result<br>No.                 | , <b>,</b>         | 7                  | m                  | 4                  | S                  | 9                  | 7   | α0                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| Q9y1x8 ephydatia f<br>Q23821 caenorhabdi<br>Q2656 schistosoma<br>Q90836 gallus gall | Oppsh2 gallus morv<br>Oppsh2 gallus gall<br>Q14256 homo sapien<br>Q923v5 rattus norv<br>P11776 xiphophorus | QBSZWI Grosophila QBpv24 xenopus lae Q99162 xiphophorus Q9njv5 biomphalari QBnjv6 oryctolagus |   | Q9ygh8 scophthalmu Q8uw83 paralichthy Q9qvw4 rattus sp. Q9vd94 drosophila Q96135 homo sapien Q91ym0 mus musculu Q99mr2 mus musculu Q07912 homo sapien |
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| Q9Y1X8<br>Q23821<br>Q26566<br>3 Q90836  | 1 Q9ESE0<br>3 Q9PSH2<br>Q14256<br>1 Q923V5<br>3 P11776   | Q9SZWI<br>3 Q9PVZ4<br>3 Q99162<br>Q9NJV5<br>Q9BG66  | 9 0                                       | 3 09YGH8<br>1 09UW83<br>09VD94<br>09VD94<br>1 091YM0<br>1 099MR2<br>007912  |
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## ALIGNMENTS

Canis familiaris (Log). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis. PEQUENCE FROM N.A.

A YOKCA H.;

SEQUENCE FROM N.A.

YOKCA H.;

SUBmitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; ABRO08451; BAA33127.1; 
REMBL; ABRO08451; BAA33127.1; 
REPROPOUS PRO00719; EKP-hand.

InterPro; IPR00174; Furin-like.

InterPro; IPR00174; Furin-like.

InterPro; IPR00174; Furin-like.

R InterPro; IPR00174; Furin-like.

R InterPro; IPR001245; Tyr\_pkinase.

InterPro; IPR001245; Tyr\_pkinase.

R Pfam; PF00757; Virin-like; 1.

R Pfam; PF00757; Yurin-like; 1.

R PF0071; PR0751 FU; 3.

SMART; SM00261; FU; 3.

SMART; SM00261; FU; 3.

R PROSITE; PS00107; PROTEIN\_KINASE\_DAP; 1.

R PROSITE; PS00107; PROTEIN\_KINASE\_DAP; 1.

R PROSITE; PS00107; PROTEIN\_KINASE\_TYR; 1.

R PROSITE; PS00107; PROTEIN\_KINASE\_TYR; 1.

M ATP-Dinding; Transferase; Tyrosine-protein kinase.

O SEQUENCE 1259 AA; 137989 WW; E37364D49CAD46 CRC64; Created)
Last sequence update)
Last annotation update) PRT; 1259 AA 01-JNN-1998 (TrEMBLrel. 05, 01-JNN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21, ErbB-2. PRELIMINARY; PARTY SERVICE TO THE PROPERTY OF THE PROPERTY

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Earp H.S.;
"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
                                                            PEYVNOPDVRPOPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGAV
                                                                                                                 PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
                                                                                                                                                        ENPEYLTPOGGAAPOPHPPPAFSPAFDNLYYWDODPPERGAPPSTFKGTPTAENPEYLGL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STAIN=FISHER; TISSUE=LIVER;
C GALTHIGGE K., Dawson T.L., Earp H.S.;
C GULTHIGGE K., Dawson T.L., Earp H.S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37394; AAF14008.1; -..
EMBL; M37394; AAF14008.1; -..
EMBL; M37394; AAF14008.1; -..
InterPro; IPR000719; Euk pkinase.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Turin-like.
InterPro; IPR001245; Turin-like.
InterPro; IPR001245; Turin-like.
IN Pfam; PF00105; Purin-like; 1.
Pfam; PF00109; Pkorinase; 1.
PR PRINTS; PR00109; Tyrkinase; 1.
PRINTS; PR00109; Tyrkinase; 1.
PROSITE; PS0010; PROTEIN KINASE ATP; 1.
PROSITE; PS0010; PROTEIN KINASE DOM; 1.
PROSITE; PS0010; PROTEIN KINASE DOM; 1.
PROSITE; PS0010; PROTEIN KINASE TYP: 1.
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STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
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Petch L.A.;
Submitted (NOV-1991) to the I
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                     PLAPSEGAGSIVVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPL 1131
                                                            1034 PLLSSLSANSN----SSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTFL---
                                                                                                                                                                                      ENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPP
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Reiter J.L., Threadgill D.W., Bley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J. Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubzamaniam S., Crossley T.O., Magnuson T.R., James C.D., Mainle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MCBI_TaxID=10090;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBL:el. 16, Last sequence update)
01-UNA-2002 (TrEMBL:el. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
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EMBL; AF275366; AAG28045.1; -
EMBL; AF275367; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; JOINED.
HSSP; P11362; 1FGK.
MGD; MG195294; EGFR.
INTEPPO; 1PR000494; EUN_FRIASE.
INTEPPO; 1PR000494; EUN_FRIASE.
INTEPPO; 1PR000179; EUN_FRIASE.
INTEPPO; 1PR001245; TYL_PKINSE.
PFGMT; PF001057; FULTIA-11Ke, 1.
PFGMT; PF00109; TYZKINASE; 1.
PFGMT; PR00109; TYZKINASE; 1.
PRINTS; PR00109; TYZKINASE; 1.
SMART; SM00220; STRC; 1.
SMART; SM00220; STRC; 1.
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                                                                                                                                                              APLICSPOPEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188
                                                                                                                                                                                                                                                                              ESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDV 945
                            -----PERG
                                                                                                     PRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLORYSEDPTVPLPSET--DGYV
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., D Altschmied J., Schartl M.;
Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations.";
Oncogene 16:1681-1690(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01030; Recep_I_domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00199; TYTCHCHROWE C; UNKNOWN 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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InterPro; IPR000494; EGFR_L domain.
InterPro; IPR000194; Buk pkinase.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF000757; Furin-like; 1.
Pfam; PF00059; pkinase; 1.
Pfam; PF00069; Recep_L domain; 2.
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STRAIN=RIO PURIFICATION;
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                                                                                                                                                                                                                      GNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVL 117
                                                                                                                                                                                                                                                                           DNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----F 173
                                                                                                                                                              57
                                                                                                                                                                                        14 LITALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSL------QRMYNNCEVVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             766 YVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYVREHKDNIGSQYLLNMCVQIAK
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                                                                                                                                                                                                                                                                                                                                   174 HKNNQLALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLP
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                                                                                                                                                                                                                                                                                                                                                     HLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCS
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                                                                                                                                                              LILLALLPPGAA-----STQVCTFNNFTVSFWLRVPKVSASHLELYQGCQVVQ
                                                                                                                                   Gaps
                                                                                                                                  132;
                                                                                                     Length 1210;
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                                                                         62CD021C9DE32E18 CRC64;
                                                                                                  PS00107; PROTEIN KINASE ATP; 1.
PS50011; PROTEIN KINASE DOM; 1.
PS00109; PROTEIN KINASE TYR; 1.
ing; Receptor; Transferase.
                                                                         134840 MW;
  CYTOCHROME
              PROSITE; PS00107; PROTE
PROSITE; PSS0011; PROTE
PROSITE; PS00109; PROTE
ATP-binding; Receptor;
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1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP 1175
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                                                                      EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
                                                                                                                                                   ---EPCIPPNGH--------PVRENSIALRYISDPTQNALEKDLDGH- 1054
                GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS
                                                                                                                          1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
                                                                                                                                                                                               ----RYKRIN-RQGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=99263203; PubMed=10328884;

MIDIACON M., Lumsdden A.;

Discribution of neuregulin-1 (nrgl) and erbB4 transcripts in embryonic chick hindbrain.";

MO1. Cell. Neurosci. 13:227-258(1999).

EMBL; AFL21963; AAD31764.1;

R SINCERPEO; IPRO00494; EGFR L domain.

R INCERPEO; IPRO00174; FULIN-like.

R INCERPEO; IPRO01309; TWFR c6.

R INCERPEO; IPRO01309; YLP motif.

R Pfam; PF001030; Furin-like; 1.

R Pfam; PF001030; Recep L domain; 1.

R Pfam; PF001030; Recep L domain; 1.
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PRO000m; PD000001; Euk_pkinase; 1.
SWART; SM00261; FU; 3.
SWART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00652; TANTE NGFR 1; UNKNOWN 1.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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ERBB4.
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NCBI_TaxID=9031;
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                                                                                                                                       1 MELAALCRWGLLLALLPPG-AAST----QVC--TFNNFTV--SFWLRVPKVSASHLELYQ 51
                                                                                                                                                                                                                                                                                                                      PLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQ
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                                                                                 Length 1165;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                            Indels
                                                                                 Query Match
40.2%; Score 2739; DB 13;
Best Local Similarity 45.9%; Pred. No. 2.3e-198;
Matches 586; Conservative 162; Mismatches 380;
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DLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLENAEYL------K 1055
                                              ----AENPEYL 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### REALLY APOSGILS, APOSG
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                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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llarity 41.2%; Pred. No. 2.1e-164;
Conservative 148; Mismatches 397;
                                                 PHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT
                                                                                                                                                                                                                   1328
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Gellner K., Brenner S.;
Analysis of 148 kb of genomic DNA
rubripes ";
Genome Res. 9:251-258(1999).
                                                                                                                                                                                                                                  P79754;
01-MAY-1997 (TrEMBLrel. 03,
01-UNA-21997 (TrEMBLrel. 03,
01-UNN-2002 (TrEMBLrel. 21,
ErbB3.
                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
Matches 510; Conserv
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                                                                                                                                                                     221 AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF
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                           Gaps
                           77;
                           Indels
    Pred. No. 1.2e-197;
; Mismatches 354;
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  Similarity 47.3%; Pr
39; Conservative 169;
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                                                                                            "Cloning, expression and localisation of the Anopheles gambiae epidermal growth factor receptor."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ301655; CAC35008.1; -HSSP; P11362; IFGK.
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InterPro; IPR000345; EdgFR L domain.
InterPro; IPR000174; EdgFR L domain.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_Pkinase.
InterPro; IPR001245; Tyr_Pkinase.
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Pfam; Pr00057; Furin-like; 1.
Pfam; Pr001057; Furin-like; 1.
Pfam; Pr001059; Recept L domain; 2.
ProDom; Pr001009; Recept L domain; 2.
ProDom; Pr001009; TYRKINASE.
ProDom; Pr001009; TYRKINASE.
INTE; PR00109; TYRK; 1.
PROSITE; PR001109; TYRC; 1.
PROSITE; PR001107; PROTEIN KINASE_DOM; 1.
PROSITE; PR001107; PROTEIN KINASE_DOM; 1.
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                WCBI_TaxID=7165;
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                    QCVNCSQFLRGQECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCV
                                                                                                                                                                                                                                                          646 QRASPLTSIVSAVVGILLVVVLGVVF-----GILIKRRQQKIRKYTMRRLLQETELVE
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BGFR.
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                                                                                                                                                                                                                                                                                                                             Henner W.D.;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Hypothetical 40.2 kD
                                                                                              MEDLINE=99415951; PubMed=10485918; Doharty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M., "The HER-2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1762.5; DB 4; Length
Pred. No. 4.7e-125;
9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                      Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., He Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AR177761, AAD560092; -- InterPro; IPR000494; EGFR. L domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027080; AAH77080.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEC1BE347E2D030C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 TSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQP 394
                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
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Pfam; PF01030; Recep L domain; 1.
SMART; SM00261; FU; 1.
SEQUENCE 419 AA; 45472 MW; FE
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Best Local Similarity 84.7%;
Matches 337; Conservative
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                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                        GCISCDKAIIGSDAKIERCLMKDESCPDGYYSDYVLQEEGPLKQLSGKAVCRKCHPRCKK
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                   494 ASEISSVLEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKMARDPPRYL 553
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                                                                                                                                                                                           RRLLQETELV3PLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK 747
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                                                                                                                            PEETATPKTG2--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCOLCHP
                                                                                                 NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
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MEDLINE=9420365; PubMed=8152791;

MEDLINE=94203659; Dibbed=8152791;

Wennstrow B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Johnsson A., Beug H.;

"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
Oncogene 91:307-1320[1994].
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
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Last annotation update)
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InterPro; IPR001245; Tyr pkinase.
Edm; PF00069; pkinase; I.
PRIMTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; I.
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EMBL; S69372; AAC60725.1;

HSSP; P03322; AAC60725.1;

Therbox.
                                                                                                                                                                                                                    61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSL
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MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
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    Length 367;
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InterPro; IPR004028; Retro M.
InterPro; IPR004028; Retro M.
InterPro; IPR00104; Tyr_pkinase.
Pfam; PF02813; Retro M; 1.
PF020m; PD000001; Buk_pkinase; 1.
SWART; SW00203; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914EFEID63 CRC64;
                                                Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11950;
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Last annotation update)
       DB 11;
25.5%; Score 1739; DB 11;
88.0%; Pred. No. 2.3e-123;
ive 11; Mismatches 33;
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Best Local Similarity 54.8%
Matches 358; Conservative
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Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R., Six amino acids from the retroviral gene gag greatly enhance th transforming potential of the oncogene Verb-B.";
Oncogene 5:15-24(1990).
-!- SIMILARITY: BELOWIGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY: EMBL; X52209; CAA36459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 WVWTCQCEPEGQVRRSPDVSSGSREGLTSAGIKRWEGPPTTSRGTCHARN 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 412;
                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

RICEPPO: IPRO20146; EF-hand.

InterPro: IPRO01245; Tyr_Dkinase.

InterPro: IPRO01245; Tyr_Dkinase.

InterPro: IPRO01245; Tyr_Dkinase.

PEam; PPO0065; Pkinase; I.

ProDom; PD00000; EF Lau, Pkinase; I.

RNOART; SM00219; TyrKc; I.

RNOSITE; PS00018; EF HAND; UNKNOWN I.

RNOSITE; PS00018; EF HAND; UNKNOWN I.

RNOSITE; PS00018; EF HAND; UNKNOWN I.

RNOSITE; PS00118; PROFEIN KINASE_DOM; I.

Hypothetical protein.

SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, v-erb-A, v-erb-B protein.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C
  Wan D.F., Gu J.R.;
"Novel human cDNA clones with function of inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%; Score 1697.5; DB 4
80.5%; Pred. No. 3.9e-120;
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Submitted (NOV-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RNGQGHPVREDSFVQ 491
                                                                                                                                                                                                                                                                                        578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 995
                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                   638 DDKGCPAEQRASPLISIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                                                             GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VEPLTPSGEAPNQAHLRILKETEFKKVKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELR
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                                                                                                                                                                                                                                           Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
                                                                                                                                                                                                                                         102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1169 RAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566
                                                                                                                                                                                            Length
                                                                                                                                                                                                                                         Indels
                                                                                                                                           567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
                                                                                                                                                                                                                                         73; Mismatches 112;
                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||
|----SRTPLLSSLSATSNNSATNCID-
                                                                                                                                                                                                                   Pred. No. 1.7e-121
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                                                                                                                                                                                          25.2%; Score 1718;
                           444
                      PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS50011; PROTEIN KINASE DOM; PROSITE; PS00109; PROTEIN KINASE TYR;
                                                                                                                                                                                                                     55.4%;
                                                                                                                                                                                                                   Best Local Similarity 55.49
Matches 357; Conservative
  SM00219; TyrKc; 1
                                                                                         ryrosine-protein kinase.
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SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE
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PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGERLPOPPICTIDUYMIMUKCWMIDSECRPRFRELUSEFSRMARDPORFVVIQ-NEDLG 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=88217326; PubMed=2897102;

Scotting P., Vennstron B., Jansen M., Graf T., Beug H., Haymann M.J.;

Scotting P., Vennstron B., Jansen M., Graf T., Beug H., Haymann M.J.;

"Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation.";

Oncogene Res. 1.265-278(1987).

EMBL: X06943; CAA30024-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTSPKANKE!!LDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000119; Euk pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Promom PD000001; Euk_pkinase; 1.
Propom PD00001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TY; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 545 AA; 60899 MW; 140DCE8CCA0F8AF4 CRC64;
                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-exbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.1%; Score 1645; DB 15;
54.9%; Pred. No. 5.5e-116;
ive 70; Mismatches 121;
                                -LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
                                                                                 961
                                                           545
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                                                                                                                                                                                                              PRELIMINARY;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 SPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1047 HRSSSTRSGGGDLTLGLEPSEERAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%; Score 1653.5; DB 15; Length 962; 51.7%; Pred. No. 2.9e-116; ive 73; Mismatches 142; Indels 119; Gaps
                                                                                                                                                                   Preserve in tryouace in tryouace in tryouace in the pfam; PF00104; hormone ref; 1.

Preserve in tryouace ref; 1.

Preserve in PF00109; pkinase; 1.

Preserve in the process of tryouace in tryouace; in the process of tryouace in the process of tryouace; in the process of tryouace in the process of tryouace; in the process of tryouace in tryouace; in the process of tryouace in tryouace in the process of tryouace in tr
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                                                                         InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrun_receptor.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001628; Znf_C4steroid.
                                                   InterPro; IPR000719; Euk pkinase.
EMBL; X52211; CAA36459.1; JOINED HSSP; P10828; 2NLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 51.7%
Matches 358, Conservative
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MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Baito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rushi P., Lawis S., Matsuo Y., Nikaido I., Reole G., Quackenbush J.,

Rochrim L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,
1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
                                  481
                                                                                         1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C3H/101, 129/SvJ, AND 129/SvEvTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Alternative Transcripts from the Human and Mouse EGFR Genes Encode
                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAN-ECSPELGG, TISSUE-LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative genomic sequence analysis and isolation of human amouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                       1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                              PRELIMINARY;
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SDCCHNQCAAGCTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFG 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 HKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 QAWPDNWTDLHAFENLEIIRGRTKQHGQFSLAVVGLNITSLGLRSLKEISDGDVIISGNR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 QFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKD 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSL-----QRMYNNCEVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 SN-----YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LILIALLEPGAA-----STQVCTFNNFTVSFWLRVPKVSASHLELYQGCQVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 DNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 VRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLVI
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588 GPHCVKTCPAGIMGENNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 PPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC
                                                                                                                                                                                                                                                                                                                                                     22.0%; Score 1500.5; DB 11; Lengt. 43.2%; Pred. No. 6.4e-105; ive 98; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                     655 AA; 72906 MW; 6B34063B1BC928CB CRC64;
                      EMEL; AK004944; BAR23688.1; --
EMEL; AK004983; BAR23688.1; --
EMEL; AK004911; BAR2364.1; --
MGD; MGT:95294; EGfr.
InterPro; IPR000494; EGFR_L domain.
InterPro; IPR002174; Furin-like.
Pfam; PP00757; Furin-like; 1.
Ffam; PP01030; Recep_L domain; 2.
SMART; SM00261; FU; 3.
AAG28047.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
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earch completed: July 22, 2003, 09:00:01 ob time : 54.3575 secs

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July 22, 2003, 08:11:38; Search time 37.9774 Seconds (without alignments) 4403.399 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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6812
1 MBLAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|    |        | Description        | Human herequlin 2 | Human tyrosine kin | HER2 transgene pla | Human HER2 (ErbB2) | HER-2/neu protein. | Human HER-2/neu on | Human HER-2/neu pr | Amino acid sequenc | Human HER-2/neu pr | HER2/neu amino aci |
|----|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|    |        | ID                 | AAY92620          | AAE12130           | AAB60167           | AAU74545           | AAW01111           | AAW92406           | AAB21198           | AAY84780           | AAB85458           | AAG88267           |
|    |        | DB                 | 21                | 22                 | 22                 | 23                 | 17                 | 20                 | 21                 | 21                 | 22                 | 22                 |
|    |        | Match Length DB ID | 1255              | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               |
| dР | Query  | Match              | 98.4              | 98.4               | 98.4               | 98.4               | 98.3               | 98.3               | 98.3               | 98.3               | 98.3               | 98.3               |
|    |        | Score              | 6700              | 6700               | 6700               | 6700               | 6694               | 6694               | 6694               | 6694               | 6694               | 6694               |
|    | Result | No.                | 1                 | 7                  | e                  | 4                  | S                  | 9                  | 7                  | 80                 | σ'n                | 10                 |

| Human Her-2/neu pr Human Her-2/neu pr Human Her-2/neu po Sequence of c-erbB Human breast cance Human breast cance Human BRR-2/neu prot Rat HER-2/neu prot Rat HER-2/neu prot Amino acid sequenc Mouse Her-2/neu on Human HER-2/neu ex Her-2/neu ex Her-2/neu ex Human ErbB2 concopt Human ErbB2 concopt Human ErbB2 corcopt Human ErbB2 corcopt Human ErbB2 corcopt Human ErbB2 corcopt Human ErbB2 extrac DC88cpv-erbB2EC fu Extracellular port Human BGF receptor Human epidermal gr Amino acid sequenc Human protein for Human protein for Human protein for | protein        |
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| AAE24067 AAE2479 AAAE2479 AAAN39568 AAAU39923 AAB211208 AAB211209 AAM51144 AAB211200 AAM51148 AAM51152 AAM51149 AAM51153 AAM51149 AAM51149 AAM51149 AAM51145 AAM51145 AAM519259 AAM519259 AAM519259 AAM50768 AAB68420  | ο <del>Σ</del> |
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suttable for the insertion of foreign T helper epitopes were identified (see features table). The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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| Alabel= insertion region
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|abel= insertion region
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 /label= Cysteine_rich_domain
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 card (CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKN 176
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EDVRLVHRDLAARNVLVKS PNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILR
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                                                                         RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV
                                    EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR
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                                                                                                                                                                                                                                                                                                                                                                                                       Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MRC; immunorapilatory; immune response; HBR-2; adoptive immunocherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                    Human tyrosine kinase-type receptor, HER-2.
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774..782
/note= "Antigenic epitope"
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced himmunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines characterised by expression of the breast cancer antigen, HBR-2. Polynucleotides that encode peptides of the invention are useful as characterised by expression of the breast cancer antigen, HBR-2. Polynuclation probes and as primers for the detection of genes of confirm transduction of polynucleotides into host cells (APCS), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HBR-2. Compounds of the invention are designed based on the HBR-2 antigenic peptide
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and pl85neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                             VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL
                                                                                           EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating tumors, particularly breast cancers, which overexpress an receptor and does not respond to an anti-ErbB antibody, comprises conjugating the antibody to a maytansinoid -
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is characterised by the overexpression of an epidermal growth factor receptor (ETbB) and does not respond or responds poorly, to treatment with an anti-ETbB antibody, comprising administering to the mammal an anti-ETbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ETbB2. The method is also useful for treating encorain, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overtan, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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/label= Intracellular domain
/note= "claimed domain, useful for immunisation"
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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95US-0414417.
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Pred. No. 0;
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                                                                                                                                                                                                                      PEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
                                                                                                                                                                                                                                      The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV
                                                      KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD
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                                                                                                                             PEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
                                  LVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLA
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                                                                                                                                                                                                                                                                                                                                                SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; hone resorption; inflammatory disease; degenerative disorder; wound healing.
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PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
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Also described are: (1) a clonal cyctocxic T lymphocyte (CTL) that is

CC culture in vitro and binds to a complex of an epitope (I), bound to a

culture an epitope antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

acids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (III) comprising (II) and apharmaceutical

excipient; (4) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic

excipient; (4) an isolated nucleic acid encoding (II). (I) has cytostatic

condimunostimilant activities, and can be used in vaccines. (I), (II)

and (III) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (I) and (III) are useful for

conditioning or evaluating an immune response to a tumour-associated

antigen when incubated with a I lymphocyte sample form a patient and

detecting the presence of bound T lymphocyte sample form a patient and

catigen when incubated with a I lymphocyte sample form a patient and

catigen when incubated with a T lymphocyte sample form a patient of

contident man and the presence of bound T lymphocyte sample form a patient

contides the prisence of bound T lymphocyte sample form a patient

contides the ability. The possible pathological side effects caused by

infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune seponse to multiple

conditions antigens from the same pathogen. Epitope-based anti-tumour

conditions antigens from the same pathogen. Epitope-based anti-tumour

conditions and the present invention antigen of tumour

culmiple tumour-associated molecules addressing the problem of tumour

culmiple antigen loss. Ang@sise to AAG@sise to AAG@sise to AAG@sise to antigen loss. AAG@sise to AAG@sise to AAG@sise to AAG@sise t
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                                  LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                      inducing
cancer -
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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                       Indels
                       6
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5; Mismatches
98.3%;
  Best Local Similarity 98.3
Matches 1237; Conservative
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                                                                                                                                                         LIPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative diseases or e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                             PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
                                                PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
                                                                                                              PEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEY
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                                                                                                                                                                         LTPQCGAAPQPHPPPAFSPAFDNLYYWDQDPPERCAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                                                                                                                                                                                           Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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Pred. No. 0;
5; Mismatches
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                                                                                                                                                                                                                                                                   standard; Protein; 1255
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8 셤 Pred. No.

98.3%;

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Best Local Similarity 98.3
Matches 1237; Conservative
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                                                           LTPQGGAAPQPHPPPARSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                                                                                                                                                                                       Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                                  1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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prevention and diagnosis of cancer, preferably breast cancer
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Mcneill PD, Vedvick TS;
                                                                                                                                                                                                             Human Her-2/neu protein.
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21-FEB-2001;
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Query Match

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1017 LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076
                                                                                                                             eliciting
                       PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQ
                                    PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRXSEDPTVPLPSETDGYVAPLTCSPQ
                                                                    PEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
                                                                                 1137 PEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines
                                                                                                                  LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                            tumour; vaccine; human;
                                                                                                                                                                                                                                                                   Human Her-2/neu oncogene-encoded p185 glycoprotein.
                                                                                                                                                                                                                                                                                                       tyrosine kinase; receptor; c-erbB2; gene therapy
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/note= "extracellular domain"
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or tea Deltapb fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, overian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 IDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKN
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98.3%; Pred. No. 0,
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Best Local Similarity 98.3
Matches 1237; Conservative
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seq4-5-25-14.rag

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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polynucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of hematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CLL), chronic myelogenous leukaemia (CLL), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
                                                                                                                                                                                                                                                                                                                       QGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAV
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Best Local Similarity 98.3%;
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                                                         RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV
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                 RRFTHQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYMIMV
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904
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  14; Indels
  Mismatches
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                           RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). X in AAR39583 represents the location of a stop codon in AAQ46083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour
cancer etc
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Pred. No. 0;
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Best Local Similarity
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        1137 PEYYNQPDVRPQPPSREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY 1196

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        Oy
        1197 LTPQGGAAPQPHPPPRSPAPDNLYYNDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

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        1197 LTPQGGAAPQPHPPPRSPAPDNLYYNDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

        Search completed: July 22, 2003, 08:40:12

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GenCore version 5.1.6
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protein search, using sw model OM protein Run on:

July 22, 2003, 08:25:54; Search time 23.0157 Seconds (without alignments) 5267.077 Million cell updates/sec

SEQ4-59-73-14 6847

1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261 Perfect score: Sequence:

**BLOSUM62** Scoring table:

283224 segs, 96134422 residues Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | •              |                            |    | SUMMARIES |                    |
|---------------|--------|----------------|----------------------------|----|-----------|--------------------|
| Result<br>No. | Score  | Query<br>Match | f<br>Query<br>Match Length | DB | QI        | Description        |
| 1             | 6707   |                | 1255                       | -  | A24571    | protein-tyrosine   |
| 7             | 5901.5 | 9              | 1254                       | ~  | .148161   | p-185 precursor -  |
| ٣             | 5901   | 86.2           | 26                         | Н  | TVRTNU    | protein-tyrosine   |
| 4             | 3098   | 'n             | 1210                       | 7  | GQHUE     | epidermal growth   |
| S             | 3074   | 44.9           | 1210                       | ~  | A53183    |                    |
| 9             | 3054.5 | 44.6           | 1223                       | Н  | TVCHLV    |                    |
| 7             | 2930.5 | 42.8           | 1308                       | ~  | A47253    | epidermal growth   |
| æ             | 2633   | 38.5           | 1166                       | Н  | 806142    |                    |
| 9             | 2373.5 | 34.7           | 1342                       | 7  | A36223    | kinase-related tra |
| 10            | 2299.5 | 33.6           | 1339                       | 7  | JC4387    | epidermal growth   |
| 11            | 1766.5 | 25.8           | 698                        |    | TVFVLV    | protein-tyrosine   |
| 12            | 1703   | 24.9           | 604                        | 7  | TVYUH     | protein-tyrosine ] |
| 13            | 1650.5 | 24.1           | 1330                       | 7  | GQFFE     | epidermal growth   |
| 14            | 1647   | 24.1           | 544                        | ~  | S35745    | protein-tyrosine   |
| 15            | 1640   | 24.0           | 545                        | ~  | 800727    | kinase-related tra |
| 16            | 1623   | 23.7           | 540                        | ~  | B44776    | protein-tyrosine 1 |
| 17            | 1621   | 23.7           | 540                        | ٦  | TVFVEB    | protein-tyrosine 1 |
| 18            | 1466   | 21.4           |                            | ~  | A36325    | epidermal growth   |
| 19            | 1274   | 18.6           | -                          | 7  | E88257    | protein let-23 (in |
| 20            | 1274   |                | 1374                       | ~  | S70712    | protein-tyrosine   |
| 21            | 1186   | 17.3           | 1369                       | 7  | S70713    |                    |
| 22            | 1121   | 16.4           | 1717                       | 7  | A45558    | epidermal growth   |
| 23            | 1086   | 15.9           | 527                        | 0  | A42032    |                    |
| 24            | 942.5  | 13.8           | 843                        | 7  | A27131    | epidermal growth   |
| 25            | 806.5  | 11.8           | 346                        | 0  | S13807    | protein-tyrosine   |
| 26            | 754.5  | •              | 311                        | N  | S13808    | protein-tyrosine   |
| 27            | 736    | 10.7           | 1363                       | N  | T43220    | insulin-like grow  |
| 28            | 720    | 10.5           | 1382                       | Н  | INHUR     | insulin receptor p |
| 29            | 713    | 10.4           | 1383                       | 7  | A36080    | insulin receptor p |

| insulin receptor p | insulin receptor-r | insulin-like growt | insulin receptor-r | protein-tyrosine k | insulin-like growt | insulin-like growt | insulin receptor - | insulin receptor - | protein-tyrosine k | insulin receptor ( | mouse developmenta | protein-tyrosine k | tyrosine kinase Mp | eph-related recept | protein-tyrosine k |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A34157             | A36502             | T43212             | B36502             | T18534             | IGHUR1             | A33837             | T30346             | A56081             | A54092             | S57245             | 148652             | 150612             | S49004             | I48953             | S05582             |
| 7                  | ~                  | N                  | N                  | 7                  | н                  | 7                  | 7                  | П                  | 7                  | 7                  | ~                  | N                  | ~                  | ~                  | ч                  |
| 1.372              | 1300               | 1607               | 1268               | 1477               | 1367               | 1371               | 1390               | 2148               | 987                | 2101               | 987                | 952                | 977                | 987                | 1114               |
| 10.4               | 10.1               | 10.1               | 6.6                | 8.6                | 9.6                | 9.6                | 9.1                | 9.0                | 0.6                | 9.0                | 8.7                | 9.8                | 9.8                | 9.8                | 8.6                |
| 712.5              | 691.5              | 691                | 680                | 670                | 699                | 658                | 623                | 618.5              | 613                | 613                | 595                | 591.5              | 589.5              | 589                | 588                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | . 43               | 44                 | 45                 |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

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protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 25-Oct-1987 #sequence\_revision 06-Dec-1996 #text\_change 11-Jun-1999
C; Accession: A24571; A25491; A44188; B44188; I59509; I57622
R; Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Akurus a19, 230-234, 1986
A; Yamamoto, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; AyTitle: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth fareference number: A24571; MUID:86118663; PMID:3003577

A; Accession: A24571

A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

?;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Y. Sero. Natl. Acad. Sci. U.S. A. 82, 6497-6501, 1985
5. Acc. Natl. Acad. Sci. U.S. A. B.
5. Title: A v-exbB-related protooncogene, G-exbB-2, is distinct from the c-exbB-1/epiderm. A: Peference number: A25491; MUID:86016729; PMID:2995967

A;Accession: A25491
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 737-1031 SEM>
A;Rosidues: 737-1031 SEM>
A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P
S;Cience 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
A;Reference number: A44188; MUID:86070181; PMID:2999974

,Accession: A44188

A;Molecule type: DNA A;Residues: 740-910 <COUI> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A; Molecule type: mRNA

A;Residues: 1-517. RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Residues: 1-517. RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Reference number: I59509

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA
A; Residues: 832-909 <REX>
A; Residues: 832-909 <REX>
A; Cross-references: GB:L23395; NID:9459807; PIDN:AAA35809.1; PID:9459808
R; Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A; Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A; Reference number: I57622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL>

774

720 714

654

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900 894

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Yamazaki, Y.; Ishikawa,
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C;Species: Mesocricetus auratus (golden hamster)
C;Species: Jesu-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y
Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1195 EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
                                                                                                                                                                                 LAPSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
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                                                                                                                                                        LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVPAFGGAVENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
                                                                                          ISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                                                                                                                                                                                                                                                                                                                                835 YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LERREFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
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                                                            VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                                                                                                                                                                                                                                                                                                    YLEDVRIVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI
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C;Superfamily: epidermal growth factor receptor; protein kinase
C;Keywords: ATP
C;Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
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A;Residues: 1-1254 <RES>
A;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1;
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86.2%; Pred. No. 2.5e-234;
tive 60; Mismatches 105; 1
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Best Local Similarity 86.2%
Matches 1088; Conservative
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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAAS8637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Comment: GDB:REBB2; NGL; NEU; HER-2
A;Cross-references: GDB:12613; OMIM:164870
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A;Mac position: 17471.1.17471.1
A;Mac position: 25/1; 75/3; 147/1; 883/3
A;Mote: the list of introns is incomplete
C;Function:
C;Function:
A;Mote: the list of introns is incomplete
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphorylation; dyladermal growth factor receptor; protein kinase erbB2 #status predicted exx.
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted exx.
F;22-1255/Momain: signal sequence #status predicted exx.
F;22-1255/Momain: EGF receptor extracellular domain repeat exer.
F;22-653/Momain: EGF receptor extracellular domain repeat exer.
F;395-605/Momain: intracellular #status predicted exx.
F;395-605/Momain: protein kinase homology exx.
F;765-734/Region: protein kinase homology exx.
F;765-734/Region: protein kinase ATP-binding motif
F;66,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;733/Active site: Lys #status predicted
F;733/Active site: Dys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr)
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Page 3

|   | TVRINU  protein-tyrosine kinase (EC 2.7.1.112) neu precurs C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 C;Accession: A24562; A61204 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. Nature 319, 226-230, 1986 A;Title: The neu oncogene encodes an epidermal gro A;Reference number: A24562; MUID:86118662; PMID:39 A;Accession: A24562 A;Molecule type: mRNA A;Residues: 1-1260 cABR> A;Crossiones: EMBL:X03362; NID:q56745; PIDN: | R;Masui, T; Mann, A.M.; Macatee, T.L.; Garland, E<br>Carcinogenesis 12, 1975-1978, 1991 A;Title: Direct DNA sequencing of the rat neu onco 2-thiazolyl!formamide or N-methyl-N-hitrosourea. A;Reference number: A61204; MUID: 92035293; PMID:16 A;Accession: A61204 A;Status: preliminary A;Molecule type: DNA A;Residues: 637-663, VV, 665-702 <mas> A;Note: authors translated the codon GCA for resid C;Genetics: C;Genetics: A;Gene: neu C;Superfamily: epidermal growth factor receptor; p C;Superfamily: epidermal growth factor duplication; F;1-19/Domain: signal sequence #status predicted.</mas> | F;20-1260/Product: protein-tyrosine kinase neu #st<br>F;658-680/Domain: transmembrane #status predicted<br>F;733-980/Domain: protein kinase homology «KIN»<br>F;731-739/Region: protein kinase ATP-binding motif<br>F;71,191,263,535,576,634/Bainding site: carbohydrat<br>F;691,Binding site: phosphate (Thr) (covalent) #st<br>F;691,Binding site: bhosphate (Thr) (covalent) #st<br>F;692/Active site: Lys #status predicted<br>F;882,1227,1253/Binding site: phosphate (Tyr) (cov<br>Query Match 86.2%; Score 5901; DB<br>Best Local Similarity 86.2%; Pred. No. 2.7e-2<br>Matches 1095; Conservative 48; Mismatches 1<br>Qy   MELAACRWGIALALLPPGAASTQVCTGTDMKLRLP<br>Db 4 MELAAWCRWGFLLALLPPGIAGTOVCTGTDMKLRLP | Qy         61 ELTYLPTNASLSFLQDIQEVQFNNFTVSFWL           Db         64 ELTYVPANASLSFLQDIQEVQGYMLIAHNQ           Qy         114 FEDNYALAVLDNGDPLANTTPVT-GASPGGLRELQL           Db         111 FEDKYALAVLDNRDPQDNVAASTPGRTPBGLRELQL           Qy         173 ILWKDIFHKANQLALTLIDTNRSRACHPCSPMCKGS           Qy         173 ILWKDIFHKANQLALTLIDTNRSRACHPCSPMCKGS           Db         171 VLWKDVFRKNNQLALTLIDTNRSRACHPCSPMCKGS |
|---|--|---|---|--|
| MELAAMCGWGLLIALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60 | DCCHEQCAAGCTGPKHSD   | 414 AWPDSLHDLSVFQNLRVİRGRVLHDGAYSLALQGLGIRWLGLRSLRELGSGLVLIHRNTH 473  480 LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSG 539  |   | 894  |
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N:CAA27059.1; PID:g56746 E.M.; Okamura, T.; Smith, R.A.; Cohen, £ cogene transmembrane domain reveals no m protein kinase homology
n; glycoprotein; phosphot
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d <TWN> if ate (Asn) (covalent) #status predicted status predicted rowth factor receptor-related protein. 3945311 PERGAPPSTFKGTPTAENPEYLGLDV 1259 s, QLRSLTBILKGGVLIQRNPQLCYQDT 172 ||||||||||||||| QLRSLTBILKGGVLIRGNPQLCYQDM 170 LPASPETHLDMLRHLYQGCQVVQGNL 60 38 #text\_change 11-Jun-1999 ovalent) #status predicted B 1; Length 1260; -234; 105; Indels 22; Gaps due 25 as Val rsor - rat 682063

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                                                                          MEHLREVRAVTSANIQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVPETLEEI
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A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
B;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396; 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification of A;Reference number: S30024; WUID:88217333; PMID:3329716
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A;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321,
',798-799,'TD',802-811,'K',813-942 <XUY>
A;Experidental source: A431 human carcinoma cells, which have large numbers of EGF recept
R;Lin, C.R.; Chen, W.S.; Krulger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.A
Science 224, 843-848, 1984
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                                                                                                                                                                                                                           rg, P.H.
Nature 309, 418-425, 1984
A,Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
A,Reference number: A00641, MUID:84219729, PMID:6328312
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A,Residues: 1-29 cHAL>
A,Cross-references: GB.M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A,Experimental source: carcinoma cell line A431-7
R,Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, Nature 309, 806-810, 1984
epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB (;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 (;Accession: A00641; A25772; $\overline{S}30024; A38672; A00642; A43615; A23062; A05281; AR;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
R:Ishii, S. Xu, Y.; Stratton, R.H.; Roe, B.A. Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human
A;Reference number: A25772; MUID:85270438; PMID:2991899
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A,Residues: 713-964 <LIN>
A,Experimental source: epidermoid carcinoma cell line A431
A,Experimental source: coldermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Ca
Biochem. Blophys. Res. Commun. 124, 125-132, 1984
A,Reference number: A23062; MUID:85046483; PMID:6093780
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A;Residues: 25-30,'S',32-51;454-467 <WEB>
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A;Residuse: 1028-1210 <SIM>
R;Weber, W; Gill, G.N.; Speiss,
Science 224, 294-297, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A; Residues: 1-1210 <ULL>
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H.S.; Jenkins, N.A.; I
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                             DLHAFENLEIIRGRIKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTI 475
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Cispecies: Mus musculus (house mouse)
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Cispecies: Musculus (house mouse)
Richetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jen Genes Dev. 8, 399-413, 1994
A;Fitle: The mouse waved-2 phenotype results from a point mutation in the ECA; Reference number: A53183; MUID:94170986; PMID:8125255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLE
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                                                                                                                         NWKKI-PGTEGOKTKI I SNRGENSCKATGOVCHALCSPEGCWGPEPRDCVSCRNVSRGREC
                                                                                                                                                                                VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                                                                               PWDQLFRNFHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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A,Residues: 1-1210 <LUE>
A,Cross-references: GB:U03425
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R:Russo, M.W.; Dukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5209 1985
A; Title: Identification of residues in the mucleotide binding site of the epidermal grow A; Reference number: A60143; MUID:85182660; PMID:298580
A;Accession: A60143; MUID:85182660; PMID:298580
A;Accession: A60143; MUID:85182660; PMID:298580
A;Accession: A60143; MUID:86182660; PMID:298580
A;Accession: A60143; MUID:8619264; PMID:298580
A;Athle: Jackson A;Accession: Associated by A;Athle: ATP-stimulated interaction between epidermal growth factor receptor and superce A;Reference number: A38023; MUID:84191554; PMID:502548
A;Athle: ATP-stimulated interaction between epidermal growth factor receptor and superce A;Reference number: A38023; MUID:84191554; PMID:5025948
A;Athle: Mustchonal independence of the epidermal growth factor receptor from a domain x A;Reference number: A3331; MUID:900333; PMID:2790960
A;Athle: Punctional independence of the epidermal growth factor receptor from a domain x A;Reference number: A3331; MUID:900333; PMID:2790960
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor C;Comment: Binding of EGF to the receptor factor acceptor; protein kinase homology
C;Comment: Binding of EGF to the receptor factor acceptor; protein kinase homology
C;Comment: Binding of EGF to the receptor factor acceptor; protein kinase homology
C;Comment: Binding of EGF to the receptor factor acceptor of c;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Comment: EGF receptor actracellular domain repeat cEGZ>
F;1-24/Domain: EGF receptor actracellular domain repeat cEGZ>
F;2-120/Promain: EGF receptor extracellular domain repeat cEGZ>
F;2-120/Promain: EGF receptor extracellular domain repeat cEGZ>
F;2-120/Promain: EGF receptor extracellular domain repeat cEGZ>
F;1-2-200/Domain: EGF receptor extracellular domain repeat cEGZ>
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F;1-2-200/Domain: EGF receptor extracellular d
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45.2%; Score 3098; DB 1; Length 1210;
Best Local Similarity 48.9%; Pred. No. 1.1e-119;
Matches 622; Conservative 180; Mismatches 356; Indels 114
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                                                            ANTINWKKLFGTPNOKTKIMNNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDCVSCONVSR
                                                                                                                             TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV
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Matches 625; Conservative 172; Mismatches 364; Indels 118;
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A47253
epidermal growth factor receptor, HER4 - human
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; Net
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/pl80erbB4, a fourth member of the epidermal g
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A;Reference number: A47253, MUID:93189574; PMID:8383326
A;Accession: A47253
A;Atstatus preliminary; not compared with conceptual translation
A;Actacus preliminary; not compared with conceptual translation
A;Residues: 1-1308 ~PLO>
A;Residues: 1-1308 ~PLO>
A;Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A;Cross-reference extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology «KIN>
F;724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                     Length 1308;
                                                                                                                                                                                                                 197;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                   Query Match 42.8%; Score 2930.5; DB 2; Best Local Similarity 44.5%; Pred. No. 8.3e-113; Matches 606; Conservative 183; Mismatches 375;
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------KNGDLQ------ALDNPEYHN 1190
                                                                                           EKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNED-L 1000
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                                                                                                            EKGERLPOPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRM 993
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EYNADGGKMPI KWMALECIHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREI PDLL
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RESULT

by the melanoma-inducing Tu locu transforming A.; Roberts protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish NyAlternate names: epidermal growth factor receptor homolog; kinase-related te Species: Xphophorus maculatus (southern platyfish)
C;Species: Xphophorus maculatus (southern platyfish)
C;Accession: Soli42; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-indu A;Reference number: S06142; MUD::90015140; PMID::2797166
A;Accession: S06142

A,Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophorus A,Reference number: S13807; MUID:91125882; PMID:1846957 A; Molecule type: DNA

A; Residues: 1-1166 <WIT>
A; Residues: 1-1166 <WIT>
A; Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
A; Crossene 6, 73-80, 1991
A; Title: Transcriptional activation of the melanoma inducing Xmrk oncoge

A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 821-1055,'N', 1027-1098,'A', 1100-1166 <ADA>
A;Residues: EMBL:X56319; NID:965284; PIDN:CAA39763.1; Accession: S13809

PID:965285

A,Map position: Y
A,Introns: 898/1; 947/1; 979/3; 1025/3; 1056/1
A,Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A,Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; E;1-25/Domain: signal sequence #status predicted <SIG>E;1-25/Domain: signal sequence #status predicted <SIG>E;5-105/Product: kinase-related transforming protein (Tu) #status predicted <MAT>E;707-972/Domain: protein kinase ATP-binding motif

tyrog

Length 1166; 38.5%; Score 2633; DB 1; 44.5%; Pred. No. 1.1e-100; Query Match Best Local Similarity

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| Matches 569; Conservative 164; Mismatches 390; Indels 156; Gaps 31; | 4 AALCRWGLLLALIPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGGQVVQGN 59 | 60 LELTYLPTNASLSFLODIQEVQFNNFTVSFWLRVPKVSASHLEQRLRIVRGTQL | : | 114 FEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTI 173 | 111 | 174 LWKDIFHKONQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-AR 232 168 NWWDITURTSNAPWHITDLALF PLANCE CARACTER PERCHCANGE CARACTER 1.1 | 233 CKGPLPTDCCHEOCAAGCTGPKHSDCIACLHPUNAGGTCHTHOPALVTVVTDTFFSMPNDF |     | 293 GRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLG 352 | 288   | 353 MEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVPETLEEI 412  146 IGSLSNTIAVNSTNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLWNLTTVKEI 405 | 413 TGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGL 47 | 406 TGYLVIMWWPENWTSLSVPQNLEIIRGRTTFSRGFSFVVVQVRHLQWLGLRSLKEVSAGN 465 | 472    | 466 VILKNTLQLRYANTINWRRLFRSEDQSIEYDARTBNQTCNNECSEDGCW-PGP 517 | 532 TQCVNCSQFLRGQECVECRVLQGLPREYVNARHCLPCHPECQDQNGSVTCFGPEADQCV 591 | 518 | 592 ACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEBGACOPCPINCTHSCVDLDDKGCPAE 651 | 652 QRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA | 637 -IVSHSSLAVGLVSGLLITVIVALLITVRVLERRRIK-RKRTIRCLLQEKELVEPLTPSGO | 712 MENGAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANK 771 | 695 | 772 EILDEAYWAGYGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNM 831 | 832 CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP 89 |        | 892 IKWMALESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP 951 | 875 I   | 95      | 935 ICTIEVYMIILKCWMIDPSSRPRFRELVGEFSQMARDPSRYLVIQGNLPSLSDRRLF | 1012 RSLLEDDDMGDLVDAERYLVPQQGFFCPDPAPGAGGWVHRRRSSSTRSGGGDLTLGLEP 1071 |
|   | 8 8   | ò   | q | ò  | g   | 8 6   | 8   | 음   | ઠે   | qq    | රු පි  | ò   | g  | ò      | q   | ò   | С   | දි දි  | ò  | g   | ò  | g   | 8 8   | ò   | d<br>d | ò  | q       | 8       | a<br>a  | පි ර  |

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Kinase_related transforming protein (erbB3) (EC 2.7.1.-) precursor - human C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C.Accession: A36223; I59164
R.Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
R.Yritle: Asian, Acad. Sci. U.S.A. 86, 9193-9197, 1989
A.Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal grA.Reference number: A36223; MUID:90083234; PMID:2687875
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A.Title: Molecular cloning and expression of another epidermal growth factor receptor-rej. A.Reference number: IS9164; MUID:90311312; PMID:2164210
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A;Map position: 12q13-12c13
D;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
1072 SEEEAPRSPIAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSET 1130
                                                       ------PVRENSITLÄNISDPTQNALEKDL 1052
                                                                                                                                                           1131 DGYVAPLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAK 1177
                                                                                                                                                                                                                                      1178 TLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERG 1237
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A,Molecule type: mRNA
A,Residues: 1-559, GY, 561-957, FY, 959-1063, 'G', 1065-1342 <RES>
A,Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
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?,707-972/Domain: protein kinase homology «KIN»
?,715-723/Region: protein kinase ATP-binding motif
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A;Molecule type: mRNA
A;Residues: 1-1342 <KRA>
A;Cross-references: GB:M29366
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                                                 CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR
                                                                                AVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA
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A; Modecule type: mRNA
A; Residues: 1-1339 <HEL>
A; Cross-references: GB: U29339; NID: 9915389; PID: 9915390
A; Experimental source: liver
A; Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue C; Comment: This protein is a functional heregulin receptor that transduces signals to the
                                                                                                                                                                                                                                                                                                                                                                    C. Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C. Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein E;1-19/Domain: signal sequence #status predicted <81G-
F;20-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F;640-659/Domain: transmembrane #status predicted <TMM>
F;705-970/Domain: protein kinase homology <KIN>
F;713-721/Region: protein kinase ATP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr) (cc
                                                                                                                                                 protein
                                                                                 C;Accession: JC4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant A;Reference number: JC4387; MUID:96096535; PMID:8522190
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                                                           #text_change 13-Nov-1998
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    rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431;
                     N'Alternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
receptor homolog
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    growth factor
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Matches 521; (
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| 3         | 514 FGGCLUSCRISKEGVCVIRCRILGGEFREFVREACCFSCRIFECLEMEGISIINGSGSUBAC 5/3                    | F; /-53/P    |
| ò         | 591 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEBGACQPCFINCTHSCVDLDDKGC 648                        | F;194-45     |
| qq        | 574 ARCAHFRDGPHCVNSCPHGILGAKGPLYKYPDAQNECRPCHENCTQGCNGPELQDCLG 631                        | F;229/AC     |
| ολ        | . 649 PAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLT 707                    | Query Pest L |
| d<br>G    | 632 QAEVLMSKPHLVIAVTVGLAVILMILGGSFLYWRGRRİQNKRAMRRYLERGESIEPLD 689                        | Matche       |
| ò         | VLGSGAFGTVYKGIWI  | ò            |
| qq        | 690 PS-EKANKVLARIFKETELRKLKVJGSGVFGTVHKGIWIPEGESIKIPVCIKVIEDKSGR 748                      | qa           |
| ò         | 768 KANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQD 827                      | δλ           |
| qq        | 749 QSFQAVTDHMLAVGSLDHAHIVRLLGGLCPGSSLQLVTQYLPLGSLLDHVKQHRFTLGPQL 808                     | qq           |
| ò         | 828 LILNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADG 887                     | λō           |
| Ωp        | 809 ILNWGVQIAKGMYYLEEHSMVHRDLALRNVMLKSPSQVQVADFGVADLLPPDDKQLLHSE 868                      | qu           |
| ò         | 888 GKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERL 947                      | ۵            |
| qq        | 869 AKTPIKWAALESIHFGKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEIPDLLEKGERL 928                      | ΩĐ           |
| ò         | 948 PQPPICTIDVYMIMVKCWMIDSECRPRELVSEFSRMARDPQREVVIQNEDLGPASPLD 1007                       | λŏ           |
| qq        | 929 AQPQICTIDUYWWWVKCWMIDENIRPTFKELANEFTRWARDPPRYLVIKRAS-GPGTP 985                        | qa           |
| ò         | 1008 STFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTL 1067                    | λō           |
| qq        | 986 PAAEPSVLTTKELQEAELEPEL  | q            |
| ờ         | 1068 GLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMG 1099  | λō           |
| Db        | 1012 DIEAEBEGGATSLGSALSLPTGTLTRPRGSQSLLSPSSGYMPWNQSSLGEACLDSAVLGG 1071                    | qa           |
| ò         | 1100 AAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQP 1143                                    | ζō           |
| qq        | 1072 REGESRPISLH-PIPRGRPASESSEGHVTGSEAELQEKVSVCRSRSRSRSPRP 1123                           | qa           |
| ò         | 1144 EYVNQPDVRPQPPSPREGP  | ò            |
| ΟÞ        | 1124 RGDSAYHSQRHSLLTPVTPLSPPGLEEEDGNGYVMPDTHLRGASSSREGTLSSVGLSSVL 1183                    | qa           |
| ò         | 1188KDVFAFGGAVENPEYLTPQGGAAPQPHPP 1216  | ð            |
| Dp        | 1184 GTEEEDEDEEYEYMNRKRRGSP-PRPP 1209   | qa           |
| RESULT 11 |   | ò            |

TVFVIV.

TVFVIV.

TVFVIV.

Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus

N;Contains: anino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jun-1999
C;Accession: B00643; A00643; AGOdwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.
C;Accession: B00643
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro
A;Reference number: A00643; MUID:8522822; PMID:2988784
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-698 «NIL»
A;Residues: 1-698 «NIL»
A;Rotoss-references: GB:M10066; GB:M138B1; NID:g211749; PIDN:AAA48763.1; PID:g211750
C;Comment: This protein is synthesized as a gag-env-erbB protein. L.B.; Raines, RESULT 11

A;Gene: gag-env-erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific F;1-6/Product: gag protein (fragment) #status predicted <GAG>

1001 1062 GGDLTLGLEPSEEBAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116 ----AFGGAVENPEYLTPQGGAAPQPHPPPAF 1219 18; 643 762 882 352 513 1117 RYSEDPTVPLESET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE 1174 116 702 172 232 822 233 EATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDN 292 942 1002 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1061 550 585 353 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE 473 LPSPTDSKFYRTLMEEDMEDIVDADEXLVPHQGFF------NSPST---SPAFDNLYYWDQ-----DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1260 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 293 IGSQYLLNWCVQIAKGMNYLEERRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGADEKE KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 584 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 644 DDKGCPAEQFASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLR 173 VEPLTPSGEAPNQAHLRILKETEFKKVKVIGSGAFGTVYKGLMIPEGEKVKIPVAIKELR ENTSPKANKEILDBAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR YHADGGKVPIXWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE ------RNGQGHPVREDSFVQ Gaps KTVFESSPYWI 2SGNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP <ERB> 80; Mismatches 137; Indels 125; 25.8%; Score 1766.5; DB 1; Length 698; 52.2%; Pred. No. 1.8e-65; Product: env protein (fragment) #status predicted <ENV>
Pyroduct: protein-tyrosine kinase erbB #status predicted
59/Domain: protein kinase homology <KIN>
10/Region: protein kinase ATP-binding motif ctive site: Lys #status predicted 1175 RAKTLSPGKNGVVKDVF-es 374; Conservative Similarity 883 1220 Match 9 703 763 823 586 634 514 local g ò g

pro

Î protein-tyrosine kinase (BC 2.7.1.112) erbB - avian erythroblastosis virus (strain C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Accession: 18-Apr.1984 #text\_change 11-Jun-1999 C;Accession: A00644; A38022 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. Cell 35, 71-78, 1983 A;Fitle: The erbB gene of avian erythroblastosis virus is a member of the src gene A;Feference number: A00644; MUID:84026539; PMID:6313229

gal

gene family

A;Accession: A00644
A;Molecule type: DNA
A;Residues: 1-604 <YAM>
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678

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A, Cross-references: FlyBase: FBgn0003731
A, Map position: 2 57F
           Species: Drosophila melanogaster
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R;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of A;Reference number: A38022; MUID:84223957; PMID:6328658
A;Accession: A38022
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
                                                                                                                                                                                                                                                                                                                                                                                                            126;
                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 1703; DB 1; Length 604; 52.2%; Pred. No. 6.1e-63; ive 76; Mismatches 128; Indels 120
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C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphoprotein extracellular #status predicted eXTP.
F; 733-764/Domain: transmembrane #status predicted eXTP.
F; 765-1330/Domain: intracellular #status predicted eINT>
F; 808-1072/Domain: protein kinase homology eXID.
F; 816-824/Region: protein kinase ATP-binding moif
F; 816-824/Region: protein kinase ATP-binding site: carbohydrate (Asn) (covalent) #status preficted
F; 714/Finding site: Lys #status predicted
F; 843/Active site: Lys #status predicted
F; 811-81/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict human epidermal growth factor re binding A:Residues: 'Å',832-866,'V',868-943,'QTPSLVK' <WAD>A;Cross-references: EMBL:X02293; NID:g7922; PIDN:CAA26157.1; PID:g929565 C;Comment: This sequence is tentative because the introns have not been identified both hormone 39; 155 215 155 | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | SERIAL | S 272 391 ---CVPCNGPCPKTCPGVTVLH------AGNIDSFRNCTVIDGNIRILDQTFSGFQDV 321 445 441 504 501 EDCQSLTRIVCAGGCA -- RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELH 273 CPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDG 333 96 156 KGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESS CPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSCPQDKMDKGGE--TORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDG--DP ASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNG AY-SLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTAN LRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSVQRGRLLGSWHGSVPYLQELQF LEORLRIVRGTOLP----EDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEIL Gaps 371; DB 1; Length 1330; Indels ö A; Molecule type: DNA A; Readdudes: 1-130 cLIV> A; Cross-references: EMBL: KO3054 R; Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, Nature: 314, 178-180, 1985 A; Title: A Drosophila genomic sequence with homology to h A; Reference number: A38021; MUID: 85137938; PMID: 2983232 Query Match 24.1%; Score 1650.5; DB 1; Best Local Similarity 30.2%; Pred. No. 1.8e-60; Matches 412; Conservative 175; Mismatches 406;

| 561<br>526<br>621 | 583                          | 629   | 688  | 746  | 806  | 950   | 923<br>1006  | 983<br>1066  | 1038  | 1092  | 1149  | 1205   |           |
|-------------------|------------------------------|---|--|--|--|---|--|--|---|---|---|--|-----------|
|                   | WGPGFTQCVNCSQFLRGQECVEECRV : | GPEADQCVACAHYKDPPFCVARCPSGVK-PDLSYMPIWKFPDEEGAC | QPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGI-LIKRRQQKI | RKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMI : | POGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLIGICLTSTVQLVTQL  :             :  :: | MPYGCILDHVRENRGRIGSQDLIAWGMOIAKGMSYLEDVRLVHRDLAARNVLVKSPN<br> | HVKITDEGLARLLDIDETEYHADGGKVPIKWMALBSILRRRFTHQSDVMSYGVTVWELMT | FGAKPYDGIPAREIPDLJEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFS | RMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFC | PDPAPCAGGMVHHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVF | DGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLFSETDGYVAPLTCSPQPEYVNQP<br>  :: : | DVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTP : | QGGAAPQPH |
| 502<br>511<br>562 | 527                          | 584   | 630  | 689  | 747  | 807   | 864<br>951   | 924  | 984   | 1039  | 1093  | 1150   | 1206      |
| Db<br>Oy<br>Db    | දු පු                        | රු අ  | රු දු  | දුරු දුරු  | & a  | \$ <del>8</del>   | & a  | \$ a   | & g   | oy<br>Op  | දු පු   | ò q  | Qy        |

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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: 0.3-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 R;Vennstroem, B. avianticed to the EMBL Data Library, March 1993 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Residues: 1-544 even. A;Residues: 1-544 even. A;Residues: 1-544 even.
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A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: oncogene; phosphotransferase; transforming protein; tyrosine-specific p
C;Reywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p
F;135-400/Domain: protein kinase homology «KIN»
F;140-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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                                                                                               Length 544;
                                                                                            24.1%; Score 1647; DB 2; Length 554.9%; Pred. No. 1.1e-60;
tive 70; Mismatches 121; Indels
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C;Accession: S00727
R;Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.
Rocogene Res. 1, 265-278, 1987
A;Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutant A;Reference number: S00727; MUID:88217326; PMID:2897102
A;Accession: S00727 virus ( kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis C;Species: avian erythroblastosis virus C;Date: 01-Dec-1989 #text\_change 28-Feb-1997

A;Molecule type: DNA A;Residues: 1-545 <SCO> A;Cross-references: EMBL:X06943

C;Genetics: A;Gene: erbB

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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superdas. ATP; phosphotransferase F;115-400/Domain: protein kinase homology <KIN>F;115-400/Domain: protein kinase homology okins
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                                                                                    24.0%; Score 1640; DB 2; Length 545; 54.9%; Pred. No. 2.1e-60; Live 69; Mismatches 122; Indels 9:
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Search completed: July 22, 2003, 09:08:10 Job time : 31.0157 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2793 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

SEQ4-59-73-14 6847 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |               |            |          |                    |                    |      |                    | •        |                  |            |          |            |          |                    |            |                    |            |            |                    |                    |          |                    |                    |                   |           |            |            |                    |                    |                    |                    |     |      |            |
|-----------|---------------|------------|----------|--------------------|--------------------|------|--------------------|----------|------------------|------------|----------|------------|----------|--------------------|------------|--------------------|------------|------------|--------------------|--------------------|----------|--------------------|--------------------|-------------------|-----------|------------|------------|--------------------|--------------------|--------------------|--------------------|-----|------|------------|
|           | Description   | g          | rattn    | Q60553 mesocricetu | P00533 homo sapien | _    | Q15303 homo sapien |          | 3388 xiphophorus | _          |          | drosop     |          | P00535 avian eryth |            | P13387 gallus gall | 8          | -          | 002466 branchiosto | P06213 homo sapien |          | P15208 mus musculu | Q9wt14 mus musculu | .4616 homo sapien |           | _          | 7          | P08069 homo sapien | Q60751 mus musculu | P24062 rattus norv | Q93105 aedes aegyp | 0   | 9208 | 4761       |
|           | Ъ             | P 0        | Ъ        | ö                  | Ъ                  | õ    | 5                  | 8        | Z                | P2         | ő        | 20         | Ы        | 2                  | Z          | H                  | P2         | Ρ7         | ဝိ                 | P0                 | П        | Ы                  | 8                  | P                 | H         | 8          | 8          | Ъ                  | õ                  | P2                 | 8                  | PS  | Ъ    | P5         |
| SUMMARIES | ID            | ERB2 HUMAN | ERB2 RAT | ERB2 MESAU         | EGFR HUMAN         |      | ERB4_HUMAN         | ERB4_RAT |                  | ERB3_HUMAN | ERB3_RAT | EGFR_DROME | ERBB_ALV | ERBB_AVIER         | ERBB_AVIEU | EGFR_CHICK         | LT23_CAEEL | ERB2_MOUSE | ILPR_BRALA         | INSR_HUMAN         | INSR_RAT | INSR_MOUSE         | IRR_MOUSE          | IRR_HUMAN         | IRR_CAVPO | MIPR LYMST | HTK7_HYDAT | IG1R HUMAN         | IG1R_MOUSE         |                    | INSR_AEDAE         |     |      | EPB4_MOUSE |
|           | DB            |            |          |                    |                    |      |                    |          | Н                |            |          |            | Н        |                    |            |                    |            |            |                    |                    |          |                    |                    |                   |           |            |            |                    | ч                  | Н                  | Н                  | -   | Н    | 7          |
|           | Length        |            | 1257     | 1254               | 1210               | 1210 | 1308               | 1308     | 1167             | 1342       | 1339     | 1426       | 634      | 604                | 540        | 703                | 1323       | 245        | 1363               | 1382               | 1383     | 1372               | 1300               | 1297              | 1300      | 1607       | 1477       | 1367               | 37                 | 1370               | 1390               | 98  | 2146 | 987        |
| a         | Query         | 8          | •        | •                  | 45.2               |      |                    | 42.5     | 38.7             | 34.8       | 33.8     | 28.0       | 25.6     | 24.9               | 23.8       | 22.7               | 18.6       | 16.7       | 10.7               | 10.5               | 10.4     | 10.4               | 10.3               | 10.2              | 10.1      | 10.1       | 8.<br>8.   | 9.6                | 9.6                | 9.6                | 9.1                | 0.6 | 0.0  | 8.7        |
|           | Score         | 6707       | 5907     | 5901.5             | 3096               | 3075 | 2930.5             | 2911     | 2649.5           | 2382.5     | 2316.5   | 1919       | 1749.5   | 1703               | 1630       | 1555               |            | 1142.5     | 736                | 718                | 713      | 712.5              | 206                | 869               | 692.5     | 691        | 670        | 699                | 629                | 655.5              | 623                | 613 | 613  | 595        |
|           | Result<br>No. | 1          | 7        | м                  | 4                  | S    | 9                  | 7        | 8                | 6          | 10       | 11         | 12       | 13                 | 14         | 15                 | 16         | 17         | 18                 | 19                 | 20       | 21                 | 22                 | 23                | 24        | 25         | 56         | 27                 | 28                 | 59                 | 30                 | 31  | 32   | 33         |

| Q07494 gallus gall<br>Q03145 mus musculu | P07949 homo sapien<br>P09759 rattus norv | P29317 homo sapien<br>P54762 homo sapien | Q91736 xenopus lae<br>O91571 xenopus lae | 000944 gallus gall<br>091738 xenopus lae | P53356 hydra atten<br>P34152 mus musculu |
|--|--|--|--|--|--|
| EPB1_CHICK<br>EPA2_MOUSE                 | RET HUMAN<br>EPBI RAT                    | EPA2_HUMAN<br>EPB1_HUMAN                 | EPBB_XENLA<br>EPBA_XENLA                 | FAK1_CHICK<br>FAK1_XENLA                 | HT16_HYDAT<br>FAK1_MOUSE                 |
|  |  |  |  |  | 77                                       |
| 984                                      | 1114                                     | 976<br>984                               | 902                                      | 1053                                     | 757<br>1052                              |
| 8 8<br>6 6                               | 8.6                                      | 8.8                                      | 8.8                                      | 8.4<br>8.3                               | 8.3                                      |
| 591.5                                    | 588<br>585                               | 584.5<br>580                             | 579                                      | 573.5<br>569                             | 567<br>563                               |
| 34                                       | 36                                       | 388                                      | 4 4                                      | 4 4<br>2 8                               | 4 4<br>5                                 |

## ALIGNMENTS

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Best Local Similarity 98.3
Matches 1240; Conservative
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111
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R InterPro; IPR000494; EGPR L domain.
R InterPro; IPR00019; Euk pkinase.
R InterPro; IPR000174; FurIn-like.
InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R Pfam; PF00109; Pkinase.
R Pfam; PF00109; Recep L domain; 2.
Pfam; PF00109; Recep L domain; 2.
R Probom; P000101; Euk pkinase; 1.
R Probom; P000101; Euk pkinase; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R PROSITE; PS00119; PROTEIN KINASE TYR; 1.
R PROSITE; PS00119; PROTEIN KINASE TYR; 1.
R PROSITE; PS00119; PROTEIN KINASE DOM; 1.
R PROSITE; PS00119; PROTEIN KINASE PRP; 1.
R PROSITE; PS00119; PROTEIN KINASE POM; 1.
R PROSITE; PS00119; PROTEIN KINASE; DOM; 1.
R PROSITE; PS00119; PROTEIN KINASE; PS00119; 
                   RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 EXTRACELLULAR (POTENTIAL).
     LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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MI1762, AAA35808.1; JG
MI1763, AAA35808.1; JG
MI1765, AAA35808.1; JG
MI1766, AAA35808.1; JG
MI1730, AAA75493.1;
MI2036, AAA35978.1;
XO3363, CAA27060.1;
                                                                                                                                                                                                                                                                                                               EMBL; M11767; AAA35808.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A25491; A25491.
PIR; A24571; A24571.
HSSP; P11362; 1FGK.
Genew; HGNC:3430; ERBB2.
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SIGNAL
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POTENTIAL
                                                                                                                                                                                                                                                                 EMBL; X03362; CAA27059.1; ALT_INIT. PIR; A24562; TVRTNU.
HSSP; P11362; 1FGR.
INCEPTO; 1FR000444; EGFR L domain.
INCEPTO; 1FR000719; EUK_EKINAGE.
INCEPTO; 1FR001745; FUTIN-1ike.
INCEPTO; 1FR00145; TYL_PKINAGE.
INCEPTO; 1FR004019; YLP_MOLIF.
PEAM; PF00069; pkinage; I.
PEAM; PF00130; Rucep L_domain; 2.
PEAM; PF02757; YLP; Z.
PRODOM; PRO00001; EUK_EKINAGE; 1.
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SMART; SM00261; FU;
SMART; SM00219; Tyrk
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SIGNAL 1
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MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM 1014
                                                                                                                                                                                                                               LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS 1140
                                                                                                                                                                                                                                                                   PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP 1200
                                                                                                                                                                                                                                                                              EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP 1260
                                                                                                                                                       MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM 1020
                                                                                                                                                                                            GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP 1080
                                                                                                                                                                                                                                           LKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYW 780
                                                                                                                              LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI 954
                                                      YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI 894
                                                                                                                   LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI 960
                                                                                                                                                                                                      GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                           AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
                                                                               YLEDVRLVHRDLAARNVLVKS PNHVKI TDFGLARLLDIDETEYHADGGKVPI KWMALESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bargmann C.I., Hung M.-C., Weinberg R.A.; "The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN 1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DTU-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185erbB2).(NEU prote-oncogene) (C-erbB-2) (Epidermal growth factor receptor related protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 852-905 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 319:226-230(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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MEDLINE-92155181; PubMed=1346763;

MEDLINE-92155181; PubMed=1346763;

Medulick W.J., Bottonley A.C., Lofts F.J., Doak D.G., Mulvey D.,

Gullick W.J., Bottonley A.C., Lofts F.J., Doak D.G., Mulvey D.,

Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;

Three dimensional structure of the transmembrane region of the proto-
orgenic and oncogenic forms of the new protein.";

EMBO J. 11:43-48 (1992).

-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ALTHOGHEN NEUREGULIN.

-!- FUNCTION: ESSENTIAL CAPPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ALPHA AND AMPHIREGULIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

-!- SUBGNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBGNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBCLILULAR LOCATION: Type I membrane protein.

-!- FUNCTION: Type I membrane protein.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE

RESIDUES. (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00219; TYTKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS500109; PROTEIN KINASE TYR; 1.

PROSITE; PS50011; PROTEIN KINASE TOW; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

Transferase, Tyrosine-protein kinase; ATP-binding; Phosphorylation;

Proto-oncogene; Disease mutation.
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CYS-RICH.
CYS-RICH.
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ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
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CVQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETBYHADGGKVP
                                                                                                           AFGGAVENPEYLVPREGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAEN
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Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
Yamazaki Y., Ishikawa T.;
Yamazaki Y., Ishikawa T.;
Goning and activation of the Syrian hamster neu proto-oncogene.";
Gene 140:251-255 (1994).
I- PUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE: GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALPHA AND AMPHIREGULIN (BY SIMILARITY).
I- CATALYTIC ACTIVITY: ATP + a protein tyrosine phosphate.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
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SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                 BILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1992 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proteo-oncogene) (C-erbB-2)
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R InterPro; IPR000419; Euk pkinase.

InterPro; IPR00174; Furin-like.

InterPro; IPR00174; Furin-like.

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R InterPro; IPR00149; YuP motif.

R Pfam; PF00157; Furin-like; 1.

R Pfam; PF00177; YuP; 2.

R Prodom; P00017; Promin: 2.

R Prodom; P0017; YuP; 2.

R SMART; SM00261; FU; 3.

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                                                Gaps
      Length 1254;
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%; Score 5901.5; DB 1;
%; Pred. No. 4.3e-307;
60; Mismatches 105;
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PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTC 1139
                                                                                                                                                                     SPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN 1199
                                                                                                                                                                                            PEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV 1259
                                                                                                                                                                                                                                                                               1194 PEYLVPRGGSASQPH-PPALCPAFDNLYYWDQDPSERGSPPNTPEGTPTAENPEYLGLDV 1252
                                                                                                                           PLAPSEGAGSDVFEGELGMGATKGPQSISPRDLSPLQRYSEDPTLPLPTETDGYVAPLAC 1133
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MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRS
                                      1014 MGDLVDAEEYLVPQQGFFFPDPAPGAGSTAHRRHRSSSTRSGGGELTLGMEPSGEEPPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGER HUMAN STANDARD; PRT; 1210 AA.
P00533; P06268; Q14225; Q9UWD7; Q9UWD8; Q9UWG5; Q92795; O00732; O00688; Q98222; Q912C9; Q9GXXI; Q9H3C9; Q9LUL-1986 (Rel. 01, created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGFR OR ERBB1.
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor receptor gene encodes a truncated form of the receptor."; Nucleic Acids Res. 24:4050-4056(1996).
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Ilekis J.V., Gariti J., Niederberger C., Scoccia B.;
"Expression of a truncated epidermal growth factor receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ilekis J.V., Stark B.C., Scoccia B.; "Possible role of variant RNA transcripts in the regulation of epidermal growth factor receptor expression in human placenta."; Mol. Reprod. Dev. 41:149-156(1995).
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"A 1.8 kb alternative transcript from the
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Gynecol. Oncol. 65:36-41(1997).
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MEDLINE=21100872; PubMed=11161793;
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MEDLINE=95382957; PubMed=7654368;
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MEDLINE=97078686; PubMed=8918811;
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MEDLINE=84219729; PubMed=6328312;
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Mammalia; Eutheria; Primates;
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
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MEDLINE-84191554; PubMed-6325948;
MROZKOWSKI B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
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                                                                                                                                                   "Comparative genomic sequence analysis and isolation of human and mouse alternative EGFR transcripts encoding truncated receptor
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Nature 309:806-810(1984).
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Haley J.D., Waterfield M.D.;
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MEDLINE=88225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
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PUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is EGF-like growth factor is call growth and differentiation. FUNCTION: Isoform 2/tuncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D., "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96398132; PubMed=8962717; Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.; "Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster
                                                                                                                                                                        Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M., Howk R., Givol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (EGF) receptor and HER2/neu are located in their carboxyl-terminal tails. Identification of a novel site in EGF receptor.";
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TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also expressed in ovarian cancers.
MISCELLANEOUS: Blanding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosaine kinase activity, stimulation of cell synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568 AND
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Growth Factors 13:121-132(1996)
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                                   ture 309:270-273(1984).
Supercoiled
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Carpenter G.;

REVIEW

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EMBL; X00588; CAA25240.1; -. EMBL; U95089; AABS3063.1; -. EMBL; U48722; AAC50802.1; -.

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                                                                           LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA
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STRAIN=BALB/C, and CD-1; TISSUB=Liver, and Decidua;
STRAIN=BALB/C, and WEDLINE-316380; PubMeda-7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts dimplantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
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Sciurognathi; Muridae; Murinae; Mus.
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
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STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=91232866; PubMed=2030916;
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Mammalia, Eutheria, Rodentia,
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STRAIN=BALB/c; TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-714 FROM N.A.
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Oncogene 7:1957-1962(1992)
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01-FEB-1996 (
01-FEB-1996 (
15-JUN-2002 (
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              'Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R MGD; MGI:95234; EgGr.

R MGD; MGI:95234; EgGr.

R InterPro; IPR00043; EGF.

L InterPro; IPR000179; Euk_Brinase.

R InterPro; IPR00179; Euk_Brinase.

R InterPro; IPR001245; Tyr_Dkinase.

R InterPro; IPR001245; Tyr_Dkinase.

R Pfam; PF00175; Furin-like; 1.

R SMART; SM00261; FU; 3.

R SMART; SM00261; FU; 3.

R SMART; SM0019; PROTEIN KINASE_ATP; 1.

R PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

R TAAISMembrane; Glycoprofein; Receptor; Signal; Transferase;

T SIGNAL.

SIGNAL.

SIGNAL.

POTENTIAL
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EMBL; U01425; AAA17899.1; -.
EMBL; XS9569; CAA42219.1; -.
EMBL; L06864; AAA53029.1; -.
EMBL; Z12608; CAA78349.1; -.
HSSP; P11362; IFGK.
                                                                                                                                      SEQUENCE OF 969-1117 FROM N.A.
                                   binding site.";
Oncogene 6:673-676(1991).
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SEQUENCE FROM N.A. (ISOFORM JM-A).

TISSUB=Breast carcinoma;

MEDLINE=93189574; Pubmed=8383326;

Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W., Foy L., Neubauer M.G., Shophab M.;

"Ligand-specific activation of HER4/pl80erbB4, a fourth member of the
                                                                                         AVVGILLVVVVLGVVFGI - LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL
                                                                                                                                                                         KETELRKVKVI.GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMA
                                                                                                                                                                                                                                                    KETEFKKIKUNGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVWA
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                                                                    VARCPSGVKPI)LSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS
                                                                                                                                                                                                                                                                                                               GVGSPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER4)
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (p180erbB4) (Tyrosine kinase-type cell surface rec
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                                                                                                                                                                                                                                                        RECEPPORS (POTENTIAL).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; JAM-4 (SHOWN HERE) AND JM-B;

ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS BXPRESSED IN THE HEART.

-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, RIDITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GIAND AND PANCREAS.

-!- THE LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R InterPro; IPR000494; EGPR L. domain.
R InterPro; IPR000494; EGPR L. domain.
R InterPro; IPR000179; Euk Ditinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR0014019; YLP motif.
R Pfam; PF00105; Pkinase.
R Pfam; PF00105; Pkorpi. 1.
R Pfam; PF00105; Pkorpi. 1.
R Prodom; P00015; Pkorpi. 1.
R SWART; SW00201; FU; 4.
SWART; SW00109; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R TRAINGEAGE (3lycoprotein); Multigene family; Receptor; Signal;
Y Traingeriase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                       "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to phorbol ester."

J. Biol. Chem. 272:26761-26768 (1997).

-!- FUNCTION: SPECIFICALLY BINDS, AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN-BINDING REF-LIKE GROWHH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                        TISSUE=Fetal brain;
MEDLINE=91476287; PubMed=9334263;
Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.
Klagsbrun M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
  epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
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CYS-RICH.
PROTEIN KINASE.
                                          SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B)
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15-JUN-2002 (Rel. 41, Last annotation update)
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                                                    YLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALI
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Q62956; Q922N7; 15-DEC-1998 (Rel. 37, Created) 15-JUN-2002 (Rel. 41, Last sequence update)

STANDARD;

ERB4\_RAT ID ERB4\_RAT

HAK I

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1031-1198 FROM N.A.
SEQUENCE OF 1031-1198 FROM N.A.
SETAAIR=Spraque-Dawley; TISSUE-Spinal cord;
MEDLINE=97184212; PubMed=9903E-Spinal
MEDLINE=97184212; PubMed=9903E-Spinal
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neureguline and their putative receptors, ErbB2 and
ErbB3, is induced duting Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997)
-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWHT FACTOR, BETARCELLUIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).
-!- CARALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTORS (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUB SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                     (EC 2.7.1.112)
                                                                                                                                                                                                         MEDLINE=98221155; PubMed=9553078; Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X., Marchionni M.A., Kelly R.A.; "Neuregulins promote survival and growth of cardiac myocytes." Neuregulins promote survival and growth of cardiac myocytes. Persistence of ExbBs and BrbB4 expression in neonatal and adult ventricular myocytes."; J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
    Receptor protein-tyrosine kinase erbB-4 precursor ERBB4 OR TYRO-2.
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR002174; Purin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR00419; YuP motif.
Pfam; PF00757; Furin-like; 1.
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MEDLINE-91222560; PubMed=2025425;
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ProDom; PD000001; Euk_pkinase; 1.
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P11362; 1FGK.
                                                             norvegicus (Rat).
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Pfam; PF01030; Recep L c
Pfam: PF02757; YLP; 7
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                                                                GC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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EXTRACELLULAR (POTENTIAL).
SMART; SM00261; FU; 4.

SMART; SM00219; TYIKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

Transmembrane; GlycoproteIn; Multigene family; Receptor; Signal;

Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
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ATP (BY SIMILARITY).
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Pred. No. 8.9e-148;
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EYLVPRECTAS:PPHPSPAFSPAFDNLYYWDONSSEOGPPPSNFEGTPTAENPEYLGLDVP 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chacesion: 148161
Ribakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Generi 140, 251-255, 1994
A;Title: 120ning and activation of the Syrian hamster neu proto-oncogene. A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene. A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Status: 148161; MUID:94193007; PMID:7908275
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1254 - REGS
A;Cross-references: GB:D16295; NID:9493236; PIDN:BAA03801.1; PID:9747595
A;Genetics:
A;Genetics:
                                                                                                               GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                                                                                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNOLA
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                                                                   LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCS
                                                                                                                                                                                                        LAPSEGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAPLACS
                                                                                                                                                                                                                                                                                                    EYLTPQGGAAFQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
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                     LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
                                                   MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDM
                                                                                                                                                                                                                                        PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP
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C; Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.8%; Score 5833.5; DE
85.3%; Pred. No. 4e-233;
tive 60; Mismatches 10
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Best Local Similarity 85.3
Matches 1075; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ 239
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                                                                                                                                                                                                                       63
                                                   (covalent) #status
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                                                                                             predicted
                                                                                                                                                           16;
F,658-680/Domain: transmembrane #status predicted <TWN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covaler F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent)
                                                                                                                                                           Indels
                                                                                                                            Score 5860; DB 1;
Pred. No. 3.3e-234;
; Mismatches 109;
                                                                                                             86.2%; Sc.
86.0%; Pred
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A;Molecule type: mRNA .
A;Residues: 'RCAMRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
A;Residues: 'RCAMRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
A;Ba-799,'TD',802-811,'R',813-942 <XUY>
A;Experimental source: A811 human carcinoma cells, which have large numbers of EGF recept R;Lin, C.R.; Chen, W.S.; Krulger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.S. Science 224, 843-848, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Modecule type: DNA
A; Residues: 1-29 cHAL>
A; Residues: 1-29 cHAL>
A; Residues: 1-29 cHAL>
A; Crose references: GB: M38425; NID: g181977; PIDN: AAA63171.1; PID: g553271
A; Experimental source: carcinoma cell line A431-7
B; Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Mer Nature 309, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs A; Reference number: A00642; MUID: 84245835; PMID: 6330563
                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-29 < LSH>
A; Residues: 1-29 < LSH>
A; Cross-references: GB:M11234; NID:g181981; PIDN:AAAS22370.1; PID:g553272
B; Haley, J.; Mittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A; Title: The human EGF receptor gene: structure of the 110 kb locus and identification of A; Reference number: $30024; MUID:88217333; PMID:3329716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplification A;Reference number: A43615; MUID:84196372; PMID:6326261
                                                        A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
A;Reference number: A00641; MUID:84219729; PMID:6328312
A;Accession: A00641
                                                                                                                                                            A;Residues: 1-1210 <ULL>
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Aan
R;Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal
A;Reference number: A25772; MUID:85270438; PMID:2991899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-29 <HA2>
A,Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature tran
A;Reference number: A38672; MUID:91107677; PMID:1988448
Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray,
                                                                                                                                                                                                                                                                                                                                                         A; Status: translation not shown
                        rg, P.H.
Nature 309, 418-425, 1984
                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                 A; Accession: A25772
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ATVVGILLFLVIGVVVGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL 715
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epidermal growt
A;Molecule type: mRNA
A;Residues: 713-964 <LIN>
A;Residues: 713-964 <LIN>
A;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley,
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 25-30, 'S', 32-51,454-467 < WEB>
B; Russo, M.W.; Luksa, T.J.; Cohen, S.; Staros, J.V.
B; Biol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleotide binding site of the A; Reference number: A60143; WUD:85182650; PMID:2985580
                                                                                                                                                                                                                                          A, Accession: A23062
A; Molecule type: mRNA
A, Redidues: 1028-1210 <SIM>
R; Weber, W. i. Gill, G. N.; Speiss, J.
Science 224, 294-297, 1984
A, Reference number: A05281; MUID:84172183; PMID:6324343
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A;Residues: 740-744,'X',746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen,
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N.Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43ē15; A23062; A05281; A60143; A33
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A,Title: Comparison of EGF receptor sequences as a guide to study the ligand binding sit. A,Reference number: A43818; MUID:91232866; PMID:2030916
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           542 LEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMG
                                                                               661 ALGIGLFMRRRHIVRKRTLRRLLQERELVEPLTPSGEAPNQALLRILKETEFKKIKVLGS
                                                                                                                                                                                                                                                                                                                    CLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAA
                                                                                                                                                                                                                                                                                                                                             CLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMYYLEDRRLVHRDLAA
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                                                                                                                                         - IGITELKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGS
                                                                                                                                                                                                                               GAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGI
                                                      DLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIQYIKANSKF---
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A;Molecule type: mRNA
A;Residues: 1-1210 <LUE>
A;Cross-references: GB:U03425
A;Cross-references: GB:U03425
Cocogene 6, 673-676, 1991
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A; Residues: 1-714 <AVI>
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A/Map position: 7p12.3-7p12.1
C/Superfamily: epidermal growth factor receptor; protein kinase homology
C/Superfamily: epidermal growth factor receptor; protein kinase homology
C/Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphorylation; duplication; glycoprotein; phosphoprotein; prosphorylation; frields and sequence #status predicted <NATY-
F/25-1210/Product: EGF receptor #status predicted <AMATY-
F/25-645/Domain: extracellular #status predicted <AMATY-
F/390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F/646-668/Domain: EGF receptor extracellular domain repeat <EE2>
F/646-668/Domain: EGF receptor extracellular domain repeat <EE2>
F/646-668/Domain: protein kinase homology <AIN>
F/10-375/Domain: protein kinase homology <AIN>
F/10-375/Domain: protein kinase ATP-binding motif
F/399-1046/Region: coated-pit mediated internalization signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status prediq
                               superco
Nature 309, 270-273, 1984

A) Title: ATP-Stimulated interaction between epidermal growth factor receptor and superc A). Title: ATP-Stimulated interaction between epidermal growth factor receptor and superc A). Reference number: A3023; MUID: 84191554; PMID: 6325948

A) Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA A; Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J Call 159, 33-43, 1989

A, Title: Functional independence of the epidermal growth factor receptor from a domain A; Reference number: A3331; MUID: 90003233; PMID: 2790960

A, Contents: annotation; internalization signal C; Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor C; Genetics:

A, Gene: GDB: EGFR
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    FAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDL

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Ribinger, D.P.; Serrero, G.
submitted to the RMEL Data Library, June 1992
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A,Reference number: A2924, X.,696-704, L.,706-70;899-992, XX',995-996, XX',998-1000;1002-1009, A,Reference number: A2924, MRN
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M.; Cell. Biol. B. 1370-1398, 1988

A;Title: Chicken epidermal growth factor [EGF] receptor: cDNA cloning, expression in mou A;Accession: A27720; MUID:88261272; PMID:3260329

A;Molecule type: mRNA

A;Residues: 1-122 cLAX>
A;Coss-references: GB:MO106

A;Molecule type: mRNA

A;Residues: 1-122 cLAX>
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro Call 41, 719-726; 1985

A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A;Residues: SGB-1223 cML>
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A;Reference number: A00643; MUID:8528222; PMID:2988784
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                                                                               Gaps
                                                  Query Match
43.0%; Score 2925.5; DB 2; Length 1308;
Best Local Similarity 45.2%; Pred. No. 2.2e-113;
Matches 608; Conservative 175; Mismatches 385; Indels 177;
C, Keywords: ATP; growth factor receptor F;716-981/Domain: protein kinase homology <KIN>F;724-732/Region: protein kinase ATP-binding motif
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N,Alternate names: epidermal growth factor receptor homolog; Kinase-related transforming C;Species: Xiphophorus maculatus (southern platyfish)
C;Species: Xiphophorus maculatus (southern platyfish)
C;Accession: S06142; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Roberts Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu loci A;Accession: S06142; MUID:90015140; PMID:2797166
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A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; P;1-25/Domain: signal sequence #status predicted <SIG>
F;25-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
F;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
----EIGHSPPPAYT 1057
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A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
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A,Residues: 1-1166 <WIT>
A,Cross-references: EMBL:X16891, NID:g65290; PIDN:CAA34770.1, PID:g65291
R,Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A,Title: Transcriptional activation of the melanoma inducing Xmrk oncoge
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38.8%; Score 2635; DB 1;
Best Local Similarity 45.0%; Pred. No. 1.8e-101;
Matches 570; Conservative 160; Mismatches 393;
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A;Residues: 821-1025,'N',1027-1098,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1131 PEYVNQPDVRPQP-----PSPRE-----GPLP-AARPAGATLERAKTLSPGKNGVVKD 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDL 1011
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                                                                                                                                                                          CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358
                                                                                                                                                                                          357 STNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLWNLTTVKEITGYLVIMWWPE 416
                                                                                                                                                                                                                                                                           SLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476
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                                                                                                                        QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298
                                                                                                                                                                                                                           359 ITEL-EFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPD 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 IPRCPHGILGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSGCRGDIVSHSSLAVGL 647
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 LEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSN 122
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                                        YQK-NPSSP--DVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWMDIVDKTSNP
                                                                                                                                        240 HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKE
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                                                                                        180 TWNLIPHAFERQCQKCDHGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGFKPIDCCNE
                                                                                                                                                                                                                                                                                                                            VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR
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                        GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL
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A;Title: Molecular cloning and expression of another epidermal growth factor receptor A;Reference number: IS9164; MUID:90311312; PMID:2164210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                                                                                                                                                                             Kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 64-0ct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession: A36223; IS9164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBBA;Title: Isolation and characterization of ERBB3, a third member of the ERBBA
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VFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-559,'G', 561-957,'F', 959-1063,'G',1065-1342 <RES>
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
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A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific p
C;Superfamily: unassigned Ser/Thr or Tyr-specific p
C;Superfamily: unassigned Ser/Thr or Tyr-specific p
C;Superfamily: unassigned Ser/Thr or Tyr-specific p
C;Superfamily: unassigned Ser/Thr or Tyr-specific p
C;Superfamily: protein kinase homology KIN>
F;715-723/Region: protein kinase ATP-binding motif
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                                                              1112 PLVSSGSMDDPDY---QAG-
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A,Molecule type: mRNA
Residues: 1-1342 < kRA>
A,Cross-references: GB:M29366
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Matches 530; Conserv
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number: JC4387; MUID:96096535; PMID:8522190

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3 LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN LOVIC ----FLLSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN 238

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ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE

**QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA** 

GDPLNNTTPVTGASPGGLRBLQLRSLTBILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL ---LNYNT----NSSHALRQLKFTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR---

LELTYLPINASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119

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120 121 180 171 239

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C,Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo_Steperfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo_Stepywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein F;10-19/Domain: signal sequence #status predicted <SIG>F;20-1339/Product: epidermal growth factor homolog #status predicted <WAT>F;40-659/Domain: transmembrane #status predicted <TWM>F;705-970/Domain: protein kinase homology <KIN>F;713-721/Region: protein kinase ATP-binding motif F;919,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr) (cc
                                                                                     Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue comment: This protein is a functional heregulin receptor that transduces signals to the
A;Reference number: JC4387; MUID:96096535; PMID:852190
A;Accession: JC4387
A;Molecule type: mRNA
A;Residues: 1-1339 cHEL>
A;Cross-references: GB:U29339; NID:g915389; PID:g915390
                                                                                                                                                                                                                                                                              Query Match
33.8%; Score 2297.5; DB 2;
Best Local Similarity 40.2%; Pred. No. 1.6e-87;
Matches 517; Conservative 170; Mismatches 433;
                                                                  A; Experimental source: liver A; Note: The authors translated the C; Comment: This protein is a functi
                                                                                                                                  A;Gene: ErbB3
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                                                                                                                                                                                                                               HGVLG--AKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTV 648
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                                                                                                                                                                                                                                                                                   FVNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNIQSWPPHMHNFS
                               VFONLOVIRGRILHNGAYS-LTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
                                                DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                                                                                        EECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                                                                                  SGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE-----QRASPLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED-----EEYEYMNRRRRHSP-PHP
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CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGL--GMQYIKANSKF
                                                                                                                                           CPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGSGSRYQTVDSSN
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                                                                                                                                                                                                       IGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWP
                                                                                                                                                                                                                                       DSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermal growth factor receptor homolog precursor - rat
N;Alternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
C;Accession: JG3387
R;Hellyer: N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.
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639 705 698

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gene family
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C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribebuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Sofence 224, 1456-1459, 1984
Sofence 224, 1456-1459, 1984
A;Title: Sequencing the erba gene of avian erythroblastosis virus reveals a new A;Reference number: A38022; MUID:84223957; PMID:6328658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERLEQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHL 473
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                                                                                                                                                                                                                                NTSPKANKEILDEAYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRL 811
                                                                                                                                                                                                                                                       234 ATSPKANKE1LDEAYVWASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNI 293
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    GP - DHCMKCAHFIDGPHCVKACPAGVLGENDTL - VWKYADANAVCQLCHPNCTRGCKGP 116
                                               691
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C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999
C;Accession: A06644; A38622
R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. Cell 35, 71-78, 1983
A;Title: The erbB gene of avian erythroblastosis virus is a member of the src A;Accession: A00644; MUID:84026539; PMID:6313229
                                                                                                                                      EPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRE
                                                                                                                                                              HAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEK
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                                               DDKGCPAEQNASPLTSIQY1KANSKF-----IGITELKRRQQKIRKYTMRRLLQETELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAFDNLYYWD()-----DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1248
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A;Residues: 1-604 <YAM>
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVFESSPYWI(SGNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
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A;Molecule type: DNA
A;Residues: 1-28, W, 30-139,'F',141-145,'V',147-152
A;Cross-references: GB:K02006
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N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Species: avian leukosis virus, ALV
C;Species: avian leukosis virus, ALV
C;Species: avian leukosis virus, ALV
C;Species: avian leukosis virus, ALV
C;Species: Doo643; Money, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.C;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.C;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.A;Reference number: A00643; MUD:85228222; PMID:2988784
A;Reference number: A00643; MUD:8528222; PMID:2988784
A;Residues: B00643
A;Residues: B00643
A;Residues: B00643
A;Residues: L698 ANIL
A;Cross-references: GB:MA10066; GB:M13881; NID:g211749; PIDM:AAA48763.1; PID:g211750
A;Residues: 1-698
A;Residues: 1-698
A;Note: in Genbank entry CHKERBBF, release 109.0, the source is designated as Gallus gal
C;Comment: This protein is synthesized as a gag-env-erbB protein.
C;Genetics:
A;Gene: gag-env-erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p
F;1-6;Product: gag protein (fragment) #status predicted <br/>F;1-59/Product: protein-tyrosine kinase erbB #status predicted <br/>F;202-210/Region: protein kinase ATP-binding motif<br/>F;229/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                     YMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLED 1005
                                                                                                                                                                                                                                                                                                                                                                                                            DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE--- 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-PIPRGR------PASESSEGHVTGSEAELQEKVSVCRSRSRSRSRSPRPRGDSAYHSQR 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1138 DVRPQPPSPREGP-----KDVARPAGATLERAKTLSP-GKNGVV-----KDVF 1179
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                                                                                                                                                                                                                                                                                                                                          ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV 945
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                                                                    ARIFKETELRKLKVLGSGVFGTVHKGIWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHM
                                          YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAK
                                                                                                                                 GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMAL
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A;Gene: FlyBase:Egfr
A;Cross-references: FlyBase:FBgn0003731
A;Gene: FlyBase:Bfr
A;Gene: FlyBase:FBgn0003731
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; glycoprotein; phosphoprotein; phosphoprotein: extracellular #status predicted <EXT>
F;1-732/Domain: extracellular #status predicted <EXT>
F;33-764/Domain: intracellular #status predicted <TWM>
F;765-1330/Domain: protein kinase homology <KIN>
F;818-824/Region: protein kinase ATP-binding motif
F;122.300,324,363,518,688,695,700/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;843/Active site: Lys #status predicted
F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
                     human epidermal growth factor red
                                                                                  A;Molecule type: DNA
A;Residues: 'A', 832-866,'V', 868-943,'QTPSLVK' <WAD>
A;Cross-references: EMBL:X02293; NID:g7922; PIDN:CAA26157.1; PID:g929565
C;Comment: This sequence is tentative because the introns have not been identified.
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A;Title: A Drosophila genomic sequence with homology to
A;Reference number: A38021; MUID:85137938; PMID:2983232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 23.8%; Score 1617.5; DB Local Similarity 29.7%; Pred. No. 1.6e-59; Nes 413; Conservative 173; Mismatches 403
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GOFFE

GOFFE

Spidermal growth factor receptor - fruit fly (Drosophila melanogaster)

N.Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;Date: 17-Nar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
C;Gocession: A00640; A38021

R;Livneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Call 40, 599-607, 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding A;Reference number: A00640; MUD:85124611; PMID:2982499
A;Accession: A00640
A;Residues: 1-130
A;Noleclib type: DNA
A;Residues: 1-130
A;Cross-references: EMBL:K03054
R;Wadsworth, G.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1115 PSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKN 1172
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                                                                                                                                                                                                                                                     RASPLTSIQYIKANSKF-----IGITELKRRQQKIRKYTWRRLLQETELVEPLTPSGAM 700
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                                                                                                                           Mismatches 135; Indels 130;
                                                                                      Length
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51.4%; Pred. No. 1.3e-61;
iive 70; Mismatches 135;
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kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus (1
C,Species: avian erythroblastosis virus
C,Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S00727
R;Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.
Oncogene Res. 1, 265-278, 1987
A;Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutants
A;Reference number: S00727; MUID:88217326; PMID:2897102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              991 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQR 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637
                                                                                                                                                                                                                                       HAEGGKVPIKWMALESILHRIYTHQSDVWSYGVIVWELMTFGSKPYDGIPASEISSVLEK 354
                                                                                                                                                                               GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRRHIVRKRTLRRLLQERELV 114
                                                                                                                                                                                                                                                                                         NTSPKANKEILDEAYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRL 811
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                                                                                                638 DDKGCPAEQRASPLTSIQYIKANSKF----IGITELKRRQQKIRKYTMRRLLQETELV
                                                                                                                                                                                                                                                                                                                                                               GSQDLLNWCMCIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEY
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                                        96;
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   Length 544;
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                      Pred. No. 2.3e-59;
64; Mismatches 128;
     23.6%; Score 1604; DB 2; 54.1%; Pred. No. 2.3e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Kerwords: ATP; phosphotransferase
F;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
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                      54.1%;
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                      Best Local Similarity
Matches 339; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1002 LLEDD---DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1110 PTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSP 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DLIGVPVSVDNPEYLLNAQTLGVGESPIPTQTIGIPVMGGPGTMEVKVPMPGS 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLG--PASPLDSTFYRS 1001
923 MSYLEEKRLVHRDLAARNVLVRLLAGEDH----DFGLAKLLSSDSNEYKAAGGKMPIKWL 978
                                                                                        ----PRSSKITA--NLDVNMI 742
                                                                                                                          FI------GITELKRRQQKIRKYT--MRRLLQETELVEPLTPSGAMPNQAQM 706
                                                                                                                                              RILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAY 766
                                                                                                                                                                                                                                                                  VMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKG 826
                                                                                                                                                                                                                                                                                                                                           MSYLEDVRLVHRDLAARNVLVK---SPNHVKITDFGLARLLDIDETEYHADGGKVPIKWM 883
                                                                                                                                                                                                                                                                                                                                                                                                                 ALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Date: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745
                                                   VK-PDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIQYIKANSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDEKDLIRKLAPTTDGSEAIAKPDDYLQPKAALGPS-----HRTDCT----
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A;Residues: 1-544 <VEN>
A;Cross-references: EMBL:X12707
C;Genetics:
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A;Accession: S35745
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1051 GDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQR 1105
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                                                                                                                                                                                                                                                                                                                   235 GSQYLLNWCVQIAKGMNYLEERHLVHRDLAARNVLVKTPQDVKITDFGLAKQLGADEKEY 294
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578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637
                                                                     638 DDKGCPAEQRASPLTSIQYIKANSKF----IĞITELKRRQQKIRKYTMRRLLQETELV 691
                                                                                                                                            692 EPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRE 751
                   1165 KTLSPGKNGVVKDVFAFGGAVENPEYL 1191
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Search completed: July 22, 2003, 09:27:20 Job time : 28.179 secs

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GenCore version 5.1.6
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protein search, using sw model OM protein Run on:

July 22, 2003, 09:10:23 ; Search time 22.1435 Seconds (without alignments) 5413.772 Million cell updates/sec

SEQ4-653-675-12 6776 1 MELAALCRWGLLIALLPPGA......TFKGTPTAENPEYLGLDVPV 1247 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | æ     |        |    | SUMMARIES |                   |
|---------------|--------|-------|--------|----|-----------|-------------------|
| Result<br>No. | Score  | Query | Length | DB | ID        | Description       |
| -             | 6602   | 97.4  | 1255   | -  | A24571    | protein-tyrosine  |
| ~             | 5809   | 85.7  | 9      | Н  | TVRTNU    | protein-tyrosine  |
| e             | 5799.5 | 85.6  | 25     | ~  | 148161    | p-185 precursor   |
| 4             | 3066   | 45.2  | 1210   | ~  | GOHUE     |                   |
| ហ             | 3032   | 44.7  | 21     | ~  | A53183    |                   |
| 9             | 3011.5 | 44.4  | 1223   | П  | TVCHLV    |                   |
| 7             | 2915.5 | 43.0  | 1308   | ~  | A47253    | epidermal growth  |
| 80            | 2596   |       | 1166   | -  | S06142    | >                 |
| 6             | 2381.5 |       | 1342   | ~  | A36223    | kinase-related tr |
| 10            | 2293.5 | 33.8  | 1339   | 7  | JC4387    | epidermal growth  |
| 11            | 1683.5 |       | 698    | 7  | TVFVLV    | protein-tyrosine  |
| 12            | 1620   | 23.9  | 604    | ч  | TVYUH     | protein-tyrosine  |
| 13            | 1612.5 |       | 1330   | П  | GOFFE     | epidermal growth  |
| 14            | 1564   | 23.1  | 544    | ~  | S35745    |                   |
| 15            | 1557   |       | 545    | ~  | 800727    | kinase-related tr |
| 16            | 1540   |       | 540    | ~  | B44776    | protein-tyrosine  |
| 17            | 1538   |       | 540    | Н  | TVFVEB    | protein-tyrosine  |
| 18            | 1509   | 22.3  | 644    | ~  | A36325    | epidermal growth  |
| 19            | 1287   |       | 1323   | ~  | E88257    | w                 |
| 20            | 1287   |       | 1374   | ~  | 870712    | protein-tyrosine  |
| 21            | 1197   |       | 1369   | ~  | 870713    | , >,              |
| 22            | 1144   |       | 71     | Н  | A45558    | epidermal growth  |
| 23            | 1126   | 16.6  | 527    | ~  | A42032    |                   |
| 24            | 975.5  |       | 843    | ~  | A27131    |                   |
| 25            | 806.5  |       | 346    | ~  | S13807    | >                 |
| 56            | 754.5  | 11.1  | 311    | ~  | S13808    | protein-tyrosine  |
| 27            | 735    |       | 36     | 7  | T43220    | insulin-like grow |
| 28            | 0      | 10.4  | 1383   | 7  | A36080    | recei             |
| 29            | 703.5  | 10.4  | 1372   | 7  | A34157    | insulin receptor  |

| insulin receptor p | insulin receptor-r | insulin-like growt | protein-tyrosine k | insulin receptor-r | insulin-like growt | insulin-like growt | insulin receptor - | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | mouse developmenta |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| INHUR              | A36502             | T43212             | T18534             | B36502             | IGHUR1             | A33837             | T30346             | A56081             | S57245             | S05582             | A54092             | 150612             | 833596             | A39753             | 148652             |
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| 1382               | 1300               | 1607               | 1477               | 1268               | 1367               | 1371               | 1390               | 2148               | 2101               | 1114               | 987                | 952                | 1091               | 984                | 987                |
| 10.3               | 10.3               | 10.2               | 10.1               | 10.0               | 9.6                | 9.4                | 9.1                | 9.1                | 0.6                | 8.8                | 8.7                | 8.7                | 8.7                | 9.8                | 8.5                |
| 701                | 695.5              | 688                | 682                | 619                | 648                | 634                | 618                | 616.5              | 610                | 593                | 591                | 587.5              | 587.5              | 580.5              | 574                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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Diotein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human NyAlternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB NyAlternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB C;Species: Homo sapiens (man)

A;Accession: A24571

A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

R,Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Toro: Natl. Acad. Sci. US.A. 82, 6497-6501, 1985
A;Title: A v-erbB-relatec protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm
A;Reference number: A25491; MUID:86016729; PMID:2995967

A, Molecule type: DNA
A, Residues: 737-1031 SEK->
A, Residues: 737-1031 SEK->
A, Residues: 737-1031 SEK->
A, Cross-references: GB:M11767; NID:9182163; PIDN:AAA35808.1; PID:9553282
A, Cross-references: GB:M11767; NID:9182163; PIDN:AAA35808.1; PID:9553282
B, Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P. Science 200, 1132-1139, 1985
A, Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A, Reference number: A44188; MUID:86070181; PMID:2999974
A, Residues: 740-910 <COUI>
A, Residues: 740-910 <COUI>
A, Residues: 1291, FALL, 522, 'S', 524-654,'V', 656-1169,'A', 1171-1255 <COU2>
A, Residues: 1-517, FALL, Aaronson, S.A.
Science 229, 974-976, 1985
A, Ring, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A, Attiel: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A, Reference number: 159509; MUID:85272597; PMID:2992089
A, Accession: 159509
A, Accession: 159509

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 832-909 <REX> A; Residues: 832-909 <REX> B; Cross-references: GB:L23395; NID: 9459807; PIDN: AAA35809.1; PID: 9459808 B; Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell. Biol. 7, 2597-2601, 1987 A; Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A; Reference number: 157622; MUID: 87286898; PMID: 3039351

A; Accession: I57622

A.Status: translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-191 <TAL>

720 772 780 832 840 892 900 952

seq4-653-675-12.rpr

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A;Gene: neu
CS;Guperfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
F;1-19/Domain: signal sequence #status predicted <81G>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
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A;Reference number: A24562; MUD:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 GBARA
A;Residues: 1-1260 GBARA
A;Residues: 1-1260 GBARA
A;Residues: 1-1260 GBARA
A;Residues: 1-1260 BABL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, B.M.; Okamura, T.; Smith, R.A.; Cohen, Carcinogenesis 12, 1975-1978, 1991
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the ran new oncogene transmembrane domain reveals no replacement number: A61204; MUID:92035293; PMID:1682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C.Accession: A24562; A61204
F.Bargmann, C.L.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
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    PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS11SAVVG
                                                     ILLVVVLGVVFGILI----QYIKANS--KFIGITEL--PLTPSGAMPNQAQMRILKETEL
                                                                                     RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKE I LDEAYVMAGVGSP
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A,Status: preliminary
A,Molecule type: DNA
A,Reddues: 637-663, V',665-702 <WAS>
A,Note: authors translated the codon GCA for residue 25 as Val
C,Genetics:
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A,Cross-references: GB:M16792, NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Gomment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Goment: GDB:ERBB2; NGL; NEU; HER-2
A;Gross-references: GDB:120613; OMIM:164870
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1, 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
C;Function:
A;Doescription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein; phosphorylation; duplication; glycoprotein; phosphorylation
C;Superfamily: epidermal growth factor receptor; protein: phosphorylation; duplication; glycoprotein; phosphorylation; catalogue predicted <SIG>F;122-1255/Product: protein-tyrosine kinase erbB2 #status predicted <AMT>F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <AMT>F;22-653/Domain: EGF receptor extracellular domain repeat <EB2>F;73-304/Domain: EGF receptor extracellular domain repeat <EB2>F;73-304/Domain: EGF receptor extracellular domain repeat <EB2>F;73-605/Domain: intracellular #status predicted <INM>F;73-605/Domain: intracellular #status predicted <INM>F;72-1255/Domain: intracellular #status predicted <INM>F;72-734/Region: protein kinase Homology <KIN>F;72-734/Region: protein kinase Homology <KIN>F;72-734/Region: protein kinase Pur-binding mocif F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;753/Active site: Lys #status predicted (Tyr) (covalent) (Dy protein kinase C) #status predicted F;753/Active site: Lys #status predicted (Tyr) (covalent) (Tyr)
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97.2%; Pred. No. 5.3e-265;
live 9; Mismatches 18;
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Best Local Similarity 97.2
Matches 1220; Conservative
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1144 YVNQSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLV 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                        D-185 precursor - golden hamster
C;Species: Mescaricetus auratus (golden hamster)
C;Species: Mescaricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161
A;Accession: 148161
                                                                                                                                                                                                      EGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAPLACSPQPE
                                                                    DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPS
                                                                                                                                      DAEEYLVPQQGFFSPDPTPGTGSTAHRRHSSSTRSGGGELTLGLEPSEGPPRSPLAPS
                                                                                                                                                                                  EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE
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     FTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
                                                     WMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
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                                                                                                                                                                                                                                                                                                                                85.6%; Score 5799.5; DB 2; Length 1254;
85.3%; Pred. No. 6.1e-232;
Live 64; Mismatches 112; Indels 9;
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A; Residues: 1-1254 cRES>
A; Residues: 1-1254 cRES>
A; Creatics:
C; Genetics:
A; Gene: neu
C; Superfamily: epidermal growth factor receptor; protein kina C; Neywords: ATP
F; 718-983/Domain: protein kinase homology cKIN>
F; 726-734/Region: protein kinase ATP-binding motif
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Matches 1070; Conservative
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                                                                                                 predicted
                                                                                                                                                                   Gaps
                                                                                                                                                                   10;
                                                                                                                                   1260;
 F;658-680/Domain: transmembrane #bcacac process.
F;723-984Domain: protein kinase homology cKIN>
F;731-739-884Domain: protein kinase homology cKIN>
F;731-191,263,535,576,634/Binding site: carbohydrate (Asn) (covaler F;71,191,263,535,576,634/Binding site: carbohydrate predicted F;759/Active site: phosphate (Thr) (covalent) #status predicted F;758/Active site: Lys #status predicted F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status ]
                                                                                                                                                                   Indels
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658-680/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                 55; Mismatches 116;
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85.6%; Pred. No. 2.5e-232;
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Best Local Simil
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Yamazaki, Y.; Ishikawa,

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A; Molecule type: DNA
A; Residues: 1-29 <HA2>
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A; Residues: 1-29 <HAL>
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                                                                                                                                                                                                                         A;Accession: S30024
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R;Ulrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.U., C.Z.,
rg, P.H.
Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of
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                                                 DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                            PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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A; Molecule type: mRNA
A; Residues: 1-1210 <ULL>
A; Residues: 1-1210 <ULL>
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
B; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
B; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
A; Title: Characterization and sequence of the promoter region of the human epidermal gro
A; Reference number: A25772.2 AUID:85270438; PMID:2991899
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A; Residues: 'RCAWRRA',150-187, 'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
A; P88-199, 'TD', 802-811,'R', 813-942 'KUTN'
A; P88-P8, 'TD', 802-811,'R', 813-942 'KUTN'
A; Experimental source: A411 hanan carcinoma calls, which have large numbers of EGF recep
B; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.
Science 224, 843-848, 1984
A; Fitle: Expression cloning of human EGF receptor complementary DNA: gene amplification
A; Reference number: A43615; MUID:84196372; PMID:6336261
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A;Redecule type: DNA
A;Residues: 1-29 <ISH>
A;Residues: 1-29 <ISH>
A;Cross-references: GBM11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
B;Haley, J; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification
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A,Residues 713-964 «LIN»
A,Residues 713-964 «LIN»
A,Experimental source: epidermoid carcinoma cell line A431
R,Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter,
R,Simmen, E.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter,
Biochem: Blophys. Res. Commun. 124, 125-132, 1984
A,Reference number: A23062; MUID:85046483; PMID:6093780
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A;Residues: 740-744, %, %, %, 46-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: APP-stimulated interaction between epidermal growth :
A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Referents: annotation; receptor activity
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R;Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson,
Nature 309, 806-810, 1984
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A; Residues: 1028-1210 <SIM>
R; Weber 2, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A; Reference number: A05281; MUID:84172183; PMID:6324343
number: A00641; MUID:84219729; PMID:6328312
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A;Residues: 25-30,'8',32-51;454-467 <WEB>
X;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 525-5208, 1985
A;Title: Identification of residues in the nucleoti
A;Reference number: A60143; MUID:85182650; PMID:298
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| double-stranded DNA  i Walton, G.M.; Der, C.J.  Qy 664 VVVLGVVFGILIQYIFANSKFIGITELPLTPSGAMPNQAQMRILKETELRKVKVL 7   | 1  | 24;  Qy   | 247<br>247<br>307<br>303 | 366<br>361<br>426<br>421  |   |
|--|--|---|--------------------------|---|---|
| A;Note: The EGF receptor (and other tyrosine kinases) can nick R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P. Cell 59, 33-43, 1980 A;Title: Functional independence of the epidermal growth factor A;Reference number: A3331; MUID:90003233; PMID:2790960 A;Contents: annotation; internalization signal C;Comment: Binding of EGF to the receptor leads to internalization commentical comments annotation; internalization signal C;Comment GB:EGF A;Cross-references: GB:120610; OMIM:131550 A;Map position: 7p12.3-7p12.1 C;Superfamilty: epidermal growth factor receptor; protein kinase C;Keywords: ATP; autophosphorylation; duplication; glycoprotein F;1-24/Domain: signal sequence #status predicted cSIG; F;25-645/Domain: EGF receptor #status predicted cSIG; F;75-300/Domain: EGF receptor extracellular domain repeat cEE; F;75-00/Domain: EGF receptor extracellular domain repeat cEE; F;66.660/Domain: GF receptor extracellular domain repeat cEE; F;66.660/Domain F;67.660/Domain  669-1210/Domain: intracellular #status predicted in 710-975/Domain: intracellular #status predicted in 710-975/Domain: protein kinase homology «KIN». 718-726/Region: protein kinase ATP-binding motif i1047-1210/Region: coated-pit mediated internalization; 1047-1210/Region: inhibitory 7128,175,352,413,444,528,603/Binding site: carbohydra; 745/Active site: Lys #status experimental  Query Match  45.2%; Score 3066; DB 1; Geet Local Similarity 49.0%; Pred. No. 2.5e-119; | vative 176 AASTQVCTC RALEBERKVCQC QEVQGYVLIAH QEVAGYVLIAH RELOLRSLTEI |                          | 308 VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARCYGLGMQYIKANSKFIGITELE-FAG 304 HGSCVRACGADSYEM-EEDGVRKCKKCEGPCRKVCNGIGIGEFK-DSLSINATNIKHFKN 367 CKKIFGSLAFLPESFDGDPASNTAPLQPEQLOVFETLEEITGYLYISAWPDSLPDLSVFG 1 | NLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLF    ::    :    :  :  :  :  :  : |

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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine Kinase (EC 2.7.1.112) erbB
N;Contains: protein-tyrosine Kinase (EC 2.7.1.112) erbB
C;Species: Galluw galluw (chicken)
C;Species: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
R;Lax, I; Johnson, A: Howk, R:; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstr Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mou A;Reference number: A27720; MUID:88261272; PMID:3260329
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A; Wolecule type: mRNA
A; Residues 1969-97. X; 973-1115, °D' < EIS>
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A; Residues 1969-97. X; 973-1115, °D' < EIS
A; Relieserant, G.J.; 611, 67.
A; Fleiserant, G.J.; 611, 67.
A; Residues 1 20 et al. 2004 A; 1019-11189.
A; Received an A2991; MUD: 89130814; PMID: 193233
A; Received an A2991; MUD: 89130814; PMID: 193233
A; Residues 1 699-697; X; 696-704; L', 706-707; 999-992, 'XX', 995-996, 'X', 998-1000, 1002-1009, R; Hibbs, M.L.; Durm, A.R.; Alexander, W.S.
B; Refibes comber: 699-694; X; 696-704; L', 706-707; 999-992, 'XX', 995-996, 'X', 998-1000, 1002-1009, R; Hibbs, M.L.; Durm, A.R.; Alexander, W.S.
A; Reference number: 695-304; M.S.
A; Reference number: 695-304; M.S.
A; Residues 1.991, X; 893-1210, VVER;
A; A; Residues 1.991, X; 893-1210, VVER;
A; A; Residues 1.991, X; 893-1210, VVER;
A; A; Residues 1.991, A; Andews, C.S.; Day, S.K.
A; Residues 1.991, A; Andews, C.S.; Day, S.K.
A; Residues 1.991, A; Andews, C.S.; Day, S.K.
A; Residues 1.991, A; Andews, C.S.; Day, S.K.
A; Residues 1.991, A; Andews, C.S.; Day, S.K.
A; Residues 1.202, 292-292, MID: 19132380; PMID: 7679348
A; Recenses 1.002, M.S.
A; Residues 1.202, 292-292, MID: 19133001; PIDN: AAA53029.1; PID: 5657201
A; Residues 1.202, RESA
A; Residues 1.202, 292-212, RESA
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C;bace Seb-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, Proc. Natl. Acad. Sci. US.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HERA/pl80erb84, a fourth member of the epid A;Reference number: A47253; MUID:93189574; PMID:8383326
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A,Accession: A27720
A,Accession: A27720
A,Accession: A27720
A,Cross-references: GB:M20386
A,Cross-references: GB:M20386
R,Nilsen, Tw. Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.Cell 41, 719-726, 1985
A,Title: c-ethB activation in ALV-induced erythroblastosis: novel RNA processing and processing. An Apacession: A00643
A,Accession: A0066
C,Generics:
A,Gene: erbB
C,Superfamily: epidermal growth factor receptor; protein kinase homology
C,Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor pecific protein kinase
F;1-1223/Product: epidermal growth factor receptor #status predicted cMT>
F;31-1223/Product: epidermal growth factor receptor #status predicted cMT>
F;31-1223/Product: epidermal growth factor receptor #status predicted cMT>
F;31-1223/Domain: Extracellular #status predicted cMT>
F;31-1233/Domain: Extracellular #status predicted cMT>
F;31-1233/Domain: intracellular #status predicted cMT>
F;31-1233/Domain: intracellular #status predicted cMT>
F;719-984/Domain: intracellular #status predicted cMT>
F;719-984/Domain: intracellular #status predicted cMT>
F;719-984/Domain: intracellular #status predicted cMT>
F;718-300-361,370,422,755,806,615,635/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;650/Binding site: phosphate (Thr) (covalent) #status predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;640/Binding site: phosphate predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;640/Binding site: phosphate (Thr) (covalent) (by protein kinase)
F;640/Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVH 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 44.4%; Score 3011.5; DB 1; Length 1223; Best Local Similarity 47.8%; Pred. No. 4.5e-117; Matches 620; Conservative 175; Mismatches 349; Indels 153;
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| 30;  | 64   | 67  | 124  | 184        | 178  | 243  | 237    | 303     | 297  | 363   | 355 | 423   | 415   | 483  | 475     | 543   | 535   | 602  | 595 | 651   | 652 | 700                         | 706  | 760  | 992   | 820   | 826 | 880  | 886  | 940  | 946   | 666   | 100   | 105   |
| h<br>Similarity 44.7%; Pred. No. 4.3e-113;<br>O3; Conservative 183; Mismatches 377; Indels 185; Gaps | WGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY | VWYSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYEN | 5 IPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN :             : : | 5 NTTPVTGA | ω    | 5 DINKSRACHPCSPMCKGSRCWGESSEDCQSLIRTVCAGGC-ARCKGPLPTDCCHEQ | 9 STNG | 4-<br>ը | 8 csópkotócracmnénosdacytocpotevýnettéolennenakýtydafecykkcehn | 4 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITEL | · > | 64 FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLXISAWPDSLPDLS | 6 FIN | 4 VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD | -><br>• | 14 QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWQPGPTQCVNCSQFLRGQECVEE | 6 TĽF | 4 CRVLQGLPREYVNARHCLPCAPECQP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPS | 9   | GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEGR | 9   | 2 TSIVSAVV-GILLVVVLGVVFGILI | 3İAAGVIGGLFILVIVGLTFAVYVRRKŠİKKKRALRRFLE-TELVEPLTF | 1 QAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVALKVLRENTSPKANKE | 07 QAQLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETVKIPVAIKILNETTGPKANVEFM | 1 DEAYWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ | 7   | 1 IAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFCLARLLDIDETEYHADGGKVPI | 7 IAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPI | B1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKDYDGIPAREIPDLEKGERLPQPPICT | IHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPI | 1 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNED-LGPASPLDSTF | 47 IDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQN | 00 *LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSE |
| Match<br>Local 8<br>les 603  |  |   | <b>6</b> 6   | 12         | 12   | 18   | 17     | 24      | 23   | 30  | 29  | 36  | 35    | 42   | . 41    | 48  | 47    | 54   | 53  | 9   | 50  | 65                          | 65   | 70   | 70  | 16  | 16  | 82   | 82   | 88   | 88  | ,<br>20   | 9   | 100   |
| Query  <br>Best L<br>Matche  | λ̈   | QQ  | <u>ک</u> ۾   | ò          | o qa | λ̈   | Db     | ٥٨      | qq   | ٥٨  | qq  | λ   | QQ    | ò  | οp      | λŏ  | Db    | ò  | qq  | à   | Db  | δ                           | QQ   | λo   | qq  | ò   | Dp  | à  | qq   | à  | qq  | à   | d<br>d  | ò   |

protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish

Nylternate names: epidermal growth factor receptor homolog; kinase-related transforming
C;Species: Xiphophorus maculatus (southern platyfish)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000
C;Accession: 806142; 813809
R;Wittbrodt, J: Adam, D:; Malitschek, B:; Maeueler, W.; Raulf, F:; Telling, A.; Roberts
R;Wittbrodt, J: Adam, D:; Malitschek, B:; Maeueler, W.; Raulf, F:; Telling, A:; Roberts
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu loc
A;Reference number: 806142; MUID:90015140; PMID:2797166
A;Roccule type: DNA
A;Residues: 1-1166 <WIT>
A;Residues: 1-1166 <WIT>
A;Residues: DNA
A;Residues: BMBL:X16891; NID:965280; PIDN:CAA34770.1; PID:965291
R;Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophoru
A;Reference number: 813807; MUID:91125882; PMID:1846957
A;Accession: 813809
A;Status: preliminary; translation not shown
A;Residues: 821-1025, NY, 1027-1098, A', 1100-1166 <ADA>
A;Cross-references: EWBL:X56319; NID:965284; PIDN:CAA39763.1; PID:965285 A;Gene: mrk
A;Gene: mrk
A;Gene: mrk
A;Gene: mrk
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; tyro
C;Superfamily: epidermal growth factor receptor; predicted <SIG>F;1-25/Domain: signal sequence #status predicted <SIG>F;2-25/Domain: signal sequence #status predicted <MAT>F;707-972/Domain: protein kinase homology <RINS
F;715-723/Region: protein kinase ATP-binding motif --PLAP-SEGAGSDVFDGDLGMGAAKGL 1090 1055 AYTPMSGNOFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKP 1114 1091 QSLPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNOPDVRPQPPS 1143 1144 PREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPP 1203 -------FSPAFDNLYYWDQDPPERGA--PPS 1227 1198 AEDEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKAFÖNPDYWNHSLPPRSTLQHPD 1257 31; 119 63 LEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSN 122 120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 59 62 8 AALLQ--LLLVLSISRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNVVLEN 60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN Indels 146; Gaps Length 1166; Query Match
38.3%; Score 2596; DB 1;
Best Local Similarity 44.2%; Pred. No. 5.6e-100;
Matches 560; Conservative 167; Mismatches 394; ---AENPEYL 1241 1258 YLQEYSTKYFYKQNGRIRPIVÄENPEYL 1285 TFKGTPT-----1060 EEAPRS-1001 1228 1168 1204 & 8 ò g ò g ò ò 셤 g \$ g 유 장 g 8

Tue Jul

| 123 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWMDIVDKTSNP 179 | 180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238  180 TWNLIPHAFERQCQKCDHGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGPKFIDCCNE 239 | 239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298  240 HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKE 299 | 299 CPYNYLSTDVGSCTLVCPLHNQEVTABDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358 | 359 ITEL-BEAGCKKIFGSLAFLPBSFDGDPASNTAPLQPEQLQVFETLBEITGYLYISAWPD 417 | 418 SLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 :: | 477 VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 536 1 | 537 GQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFC 596 | S97 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656 : | 657 AVVGILLVVVLGVVFGILIQYIKANSKFIGITELPLTPSGAMPNQAQMRILKE 709 647 LVSGLLITVIVALLIVVILRRRRIKRKRTIRCLLQEKELVBPLTPSGQAPNQAPLRILKE 706 | 710 TELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGV 769<br> | 770 GSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLE 829 16 | 830 DVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRR 889<br>: | 890 RFTHQSDVWSYGVTVWELMTFGAKFYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVK 949 | 950 CWMIDSECRPREELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDL 1009 | 1010 VDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP 1069 | SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVAPLTCSPQ 112 |     | 1129 FBIVNQFUVKEQKSPKKESPLK-ARKFAGATLEKAKTLSFGKNGVVKD 1175 | 1176 VFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTA 1235<br> |
|--|--|--|--|--|---|--|--|--|--|--|---|---|--|--|--|--|-----|--|--|
| ,<br>বু  | <u>ئ</u> ۾   | oy<br>Oy   | Oy<br>Dp   | oy<br>G  | λ<br>Q  | Qy<br>Dp   | oy<br>Oy   | oy<br>B  | Qy   | Qy<br>Dp   | oy<br>B   | c<br>S<br>S   | <u>ک</u> ۾   | 6y<br>Dp   | à a  | ò á  | 3 2 | <u> </u>   | Qy<br>Db   |

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kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human C;Species: Homo sapiens (man)
C;Date: 04-Oct.1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession: A36223; IS9164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal g A;Reference number: A36223; MUID:90083234; PMID:2687875
A;Accession: A36223
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-1342 <KRA>
A;Cross-references: GB:M29366
A;Cross-references: GB:M29366
R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J
Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-re
A;Reference number: I59164; MUID:90311312; PMID:2164210
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AjCross-references: GDB:119880; OMIM:190151
AjCross-references: GDB:119880; OMIM:190151
AjCross-references: GDB:119880; OMIM:190151
Cj.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo Cj.Keywords: ATP; phosphotransferase
Cj.Keywords: ATP; phosphotransferase
F;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
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A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
C;Genetics:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                          TKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSRGGVCV
                                                                  EECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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N;Alternate names: ErbB3 protein; HER3 protein
C;Species: Rattues norvegicus (Norway rat)
C;Species: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 1
C;Accession: JC4387
C;Accession: JC4387
C;Accession: JC4387
C;Accession: JC4387
C;Accession: JC4387; MUD:96096535; PMID:8522190
A;Title: Cloning of the rat ErbB3 cDNA and characterization of th
A;Referênce number: JC4387; MUD:96096535; PMID:8522190
A;Accession: JC43387
A;Molecule type: mRNA
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A;Cross-references: GB:U29339; NID:g915389; PID:g915390
A;Experimental source: liver
A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
C;Comment: This protein is a functional heregulin receptor that transduces signals to th
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Pred. No. 1.9e-87;
3; Mismatches 430;
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Best Local Similarity 40.3%; Pre
Matches 517; Conservative 173;
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| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRRHIVRKRTLRRLLQERELV 173  Qy 691 -PLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRE 749 | Db 234 ATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNI 293  Qy 810 GSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEY 869  Db 294 GSQYLLNWCVQIAKGMNYLEBRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGADEKEY 353 | Qy         870 HADGGKVPIKMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEK 929           D         354 HAEGGKVPIKWALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEK 413           Qy         930 GERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGP 988 | 989<br>474<br>1049   |  | OY 1162 AKTLSPGKNGVVKDVFAFGGAVENDEYLTPQGGAAPQPHPPPAFS 1206   | RESULT 12  TVVUI  protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)  C;Species: avian erythroblastosis virus  C;Species: avian erythroblastosis virus  C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999  C;Accession: A00644; A38022  R;Yanamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.  Cell 35, 71-78, 1983  A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene famil  | A; Arcestone number: A00644; MUID:84026539; PMID:6313229 A; Accession: A00644 A; Molecule type: DNA A; Moseduse: 1-604 · CAMA A; Residuse: 1-604 · CAMA A; Cross - Cameron - Cam | A; Modecute type: UNA A; Residues: 1-28, W', 30-139,'F',141-145,'V',147-152 < DEB> A; Cross-references: GB:K02006 A; Canetics: A; Genetics: C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;130-1395/Domain: protein kinase homology < KIN> F;130-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted   |
|---|---|--|--|--|--|--|--|---|
| PLGS TDPG ADFG  | Db 881   HFGKYTHQSDVWSYGVTVWELMIFGAEPYAGLRLAEIPDLLEKGERLAQPQICTIDVYM 940  Qy 946 IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1005  | QY         1006 MGDLVDAEBYLVPQQGFFCPDPAPGAGGMVHRRRSSTRSGGGDLTLGLEPSEE 1060           bb         998 LQEABLEPEL   | 1098 PSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 113  1088 PSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 113  1088 PSPLQRYSEDPTVPLPSETSESEGHVTGSEAELQEKVSVCKSRSRSRSPRPRGDSAYHSQRHS 113  1138 RPQPPSFREGPLPAARPAGATLERAKTLSP-GKNGVVKDVFAF 117 |  | TVFVLV protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus (5.8pecies: avian leukosis virus, ALV (5.8pecies: avian leukosis virus, ALV (5.8pecies: avian leukosis virus, ALV (5.8pecies: avian leukosis virus, ALV (5.8pecies: 13bec-1991 #sequence_revision 31bec-1991 #text_change 11-Jun-1999 (5.8ccession: B00643; A00643 (6.8) (7.8 | A; Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A; Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A; Reference number: A00643; MUID: 85228222; PMID: 2988784 A; Accession: B00643 A; Molecule type: mRNA A; Residues: 1-698 «NIL» A; Residues: 1-698 «NIL» A; Ross-references: GB:M10066; GB:M13881; NID: G211749; PIDN: AAA48763.1; PID: G211750 A; Note: in Genbank entry CHKERBBF, release 109.0, the source is designated as Gallus gal C; Comment: This protein is synthesized as a gag-env-erbB protein. | Gene: ge<br>Gene: ge<br>Gene: ge<br>Keyworde<br>1-6/Proc<br>7-59/Proc<br>60-698/E<br>194-459/<br>202-210/  | Query Match         24.8%; Score 1683.5; DB 1; Length 698;           Best Local Similarity         50.6%; Pred. No. 1.4e-62;           Matches 362; Conservative 82; Mismatches 140; Indels 131; Gaps 20;           Qy         578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637           Db         60 GPDHCMKCAHFIDGPHCVACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP 116           Db         638 DDKGCPAEQRASPLTSIVSAVV-GILLUVVLGVVFGILIQYIKANSKFIGITEL- 690           Qy         638 DDKGCPAEQRASPLTSIVSAVV-GILLUVVLGVVFGILIQYIKANSKFIGITEL- 690 |

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A; Kesiques: A', 832-80b, '', 804-943, 'Urbalvn' kwal)
A; Cross-references: EMBL:X02293; NID:97922; FIDN:CAA26157.1; PID:999565
C; Comment: This sequence is tentative because the introns have not been identified.
C; Genetics:
A; Gene: FlyBase:Egfr
A; Cross-references: FlyBase:FBgn0003731
A; Map position: 2 57F
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Reywords: ATP; autophosphorylation; duplication; glycoprotein; phosphory C; Reywords: ATP; autophosphorylation; duplication; glycoprotein; phosphory F; 1-732/Domain: extracellular #status predicted <EXT>
F; 733-764/Domain: intracellular #status predicted <INT>
F; 733-764/Domain: intracellular #status predicted <INT>
F; 816-824/Region: protein kinase Amp-binding motif
F; 122,100,103,24,535,518,688,695,700(Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 843/Active site: Lys #status predicted
F; 843/Active site: Lys #status predicted
F; 1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                          Query Match 23.8%; Score 1612.5; DB 1; Length 1330; Best Local Similarity 29.6%; Pred. No. 2.1e-59; Matches 409; Conservative 175; Mismatches 413; Indels 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYK----DPPF---
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   type: DNA
'A',832-866,'V',868-943,'QTPSLVK'
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NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
C;Accession: A00640; A38021
R;Litureh, B. 2. (3 Lazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Cell 40, 599-607, 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding
A;Accession: A00640
A;Accession: A00640
A;Molecule type: DNA
A;Residues: 1-130 cLIV>
A;Residues: 1-130 cLIV>
A;Cross-references: EMBL:K03054
A;Cross-references: EMBL:K03054
A;Cross-references: EMBL:K03054
A;Title: A Drosophila genomic sequence with homology to human epidermal growth factor re
A;Reference number: A38021; MUID:85137938; PMID:2983232
A;Accession: A38021
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                                                                                        RASPLTSIVSAVV-GILLVVVLGVVFGILI--QYI---KANSKFIGITEL--PLTPSGAM
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                                   132;
23.9%; Score 1620; DB 1; Length 6(
50.5%; Pred. No. 4.9e-60;
ive 78; Mismatches 131; Indels
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Kinase-related transforming protein (erbB) (EC 2.7.1..) - avian erythroblastosis virus (Cispecies: avian erythroblastosis virus Cispecies: avian erythroblastosis virus (Cispecies: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 Ciscocasion: 800727 Riscotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J. A;Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutant A;Reference number: 800727; MUID:88217326; PMID:2897102
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   578 GPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDL
                                      115 EPLTPSGEAPNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELRE
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A;Cross-references: EMBL:X06943
C;Genetics:
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C;Species: avian erythroblastosis virus
C;Species: avian erythroblastosis virus
C;Species: avian erythroblastosis virus
C;Species: 33745
B;Vannstroem, B.
submitted to the BMBL Data Library, March 1993
A;Reference number: S35745
A;Accession: S35745
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23.1%; Score 1564; DB 2; Length 544;
Best Local Similarity 53.1%; Pred. No. 9e-58;
Matches 333; Conservative 72; Mismatches 124; Indels 9:
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1104 YSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LERA 1162
                                                                                                                                                                                                                                                                                                                       1049 GDLTLGLEPSEEBAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQR 1103
                                                                                                                                                                                  355 GERLPQPPICTIDVYMIMVXCWMSDADSRPKFRELIAEFSKWARDPPRYLVIQGDERWHL 414
                                                                                                                                                                                                                                                                                                                                        691 -PLTPSGAMPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRE 749
                                                          750 NTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRL 809
                                                                                                       175 ATSPKANKEILDEAYVWASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNI 234
                                                                                                                                       810 GSQDLLINWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEY 869
                                                                                                                                                    235 GSQYLLNWCVQIAKGMNYLEERHLVHRDLAARNVLVKTPQDVKITDFGLAKQLGADBKEY 294
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Search completed: July 22, 2003, 09:27:34 Job time : 28.1435 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

July 22, 2003, 09:10:23 ; Search time 22.2855 Seconds (without alignments) 5413.772 Million cell updates/sec

SEQ4-695-709-12

Perfect score:

6815 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

283224

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMIS

|           | Description    | protein-tvrosine k | protein-tyrosine k | p-185 precursor - | mal   |        |        | epidermal growth f | $\rightarrow$ | kinase-related tra | epidermal growth f |        | protein-tyrosine k | protein-tyrosine k | kinase-related tra | · epidermal growth f | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        | growth | ~      | protein-tyrosine k | insulin-like growt | insulin receptor p |        |
|-----------|----------------|--------------------|--------------------|-------------------|-------|--------|--------|--------------------|---------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|----------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------|
| SUMMARIES | ID             | A24571             | TVRTNU             | 148161            | GQHUE | A53183 | TVCHLV | A47253             | S06142        | A36223             | JC4387             | TVFVLV | TVYUH              | S35745             | S00727             | GQFFE                | B44776             | TVFVEB             | A36325             | E88257 | S70712             | S70713             | A45558             | A42032 | A27131 | S13807 | S13808             | T43220             | 9                  | A34157 |
|           | DB             | ¦                  | Н                  | 0                 | Н     | ~      | Н      | ~                  | Н             | ~                  | ~                  | Н      | Н                  | N                  | N                  | 7                    | N                  | Н                  | ~                  | N      | 0                  | 0                  | Н                  | 0      | ~      | N      | N                  | N                  | ~                  | 7      |
|           | Length         | 1255               |                    |                   |       |        |        |                    |               |                    | 1339               | 698    | 604                | 544                | 545                | 1330                 | 540                | 540                | 644                | 1323   | 1374               | 1369               | 1717               | 527    | 843    | 346    | 311                | 1363               | 1383               | 1372   |
| d         | Query<br>Match | 97.4               | 85.7               | 85.6              | 45.0  | 44.6   | 44.2   | 42.4               | 38.1          | 34.2               | 33.0               | 24.7   | 23.8               | 23.1               | 23.0               | 23.0                 | 22.8               | 22.7               | 22.1               | 18.2   | 18.2               | 17.0               | 16.6               | 16.5   | •      |        | 11.1               | 0                  | 9.8                | 9.8    |
|           | Score          | 6640               | 5843               | 5833.5            | 3067  | 3038   | 3014.5 | 2887.5             | 2598          | 2332.5             | 2246.5             | 1686.5 | 1623               | 1575               |                    | 1565.5               | 1551               | 1549               | 1509               | 1243   | 1243               | 1160               | 1134               | 1126   | 975.5  | 806.5  | 754.5              | 700                | 999                | 665.5  |
|           | Result<br>No.  | -                  | 7                  | m                 | 4     | ഗ      | 9      | 7                  | 80            | σ                  | 10                 | 11     | 12                 | 13                 | 14                 | 15                   | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22                 | 23     | 24     | 25     | 5,6                | 27                 | 28                 | 29     |

|   | insulin receptor p | protein-tyrosine k | insulin receptor-r | insulin-like growt | insulin receptor-r | insulin-like growt | insulin receptor - | insulin receptor - | insulin receptor ( | insulin-like growt | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | tyrosine kinase Mp | protein-tyrosine k | protein-tyrosine k |
|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   | INHUR              | T18534             | A36502             | T43212             | B36502             | 1GHUR1             | A56081             | T30346             | S57245             | A33837             | A54092             | S05582             | 150612             | S49004             | A39753             | A36355             |
|   | 7                  | 7                  | 7                  | N                  | 7                  | п                  | П                  | 7                  | 7                  | 7                  | ~                  | ٦                  | ~                  | 7                  | 7                  | 7                  |
|   | 1382               | 1477               | 1300               | 1607               | 1268               | 1367               | 2148               | 1390               | 2101               | 1371               | 987                | 1114               | 952                | 217                | 984                | 916                |
|   | 7.6                | 7.6                | 9.6                | 9.6                | 9.3                | 89<br>99           | 8.8                | 8.7                | 8.7                | 9.8                | 8.4                | 8.3                | 8<br>.3            | 8.3                | 8.2                | 8.1                |
|   | 664                | 658                | 656.5              | 655                | 636                | 602                | 596.5              | 591                | 290                | 583                | 572                | 565                | 563.5              | 562.5              | 5.095              | 552.5              |
| • | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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| nase                       | 440                                       |
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NiAlternate names: c-erb.B-2 protein precursor; kinase-related transforming protein erbB C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999
C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999
C;Accession: A2571; A25411; Ā41189; B44188; I59509; I57622
R;Yamamoto, T; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f A;Reference number: A24571; MUID:86118663; PMID:3003577

A; Accession: A24571

A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Yoco, Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-exbB-related protooncogene, c-exbB-2, is distinct from the c-exbB-1/epiderm
A;Reference number: A25491; MUID:86016729; PMID:2995967

A;Accession: A25491 A;Wolecule type: DNA A;Residues: 737-1031 <SEM> A;Cross-references: GE:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 A;Cross-references: GE:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P Science 230, 1132-1139, 1985

A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A;Reference number: A44188; MUID:86070181; PMID:2999974 A;Accession: A44188

A;Molecule type: DNA A;Residues: 746-910 <COU1> A;Cross.references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A; Molecule type: mRNA A; Residues: 1.517, RALL', 522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2> A; Cross. references: GB:M11730; NID:9183986 A; King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985 A; Fitle: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A; Reference number: 159509; MUID:85272597; PMID:2992089

A;Status: translated from GB/EWBL/DDBJ
A;Status: translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 832-909 cREX
A;Cross-references: GB:L22395; NID:9459807; PIDN:AAA35809.1; PID:9459808
B;Tal. M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A;Reference number: 157622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL> A;Accession: I57622

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A;Cross-references: GB:W16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Genetics:
C;Gentics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Cross-references: GDB:120613; OMIM:164870
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorotein, phosphorotein, phosphorotein, protein-tyrosine kinase erbB2 #status predicted *RTP-
C;Superfamily: epidermal growth factor accellular domain repeat *EB1->
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted *RTP->
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted *RTP->
F;22-653/Domain: EGF receptor extracellular domain repeat *EB2->
F;22-653/Domain: EGF receptor extracellular domain repeat *EB2->
F;30-605/Domain: EGF receptor extracellular domain repeat *EB2->
F;30-605/Domain: intracellular #status predicted *TWP->
F;30-605/Domain: protein kinase ATP-binding motif
F;68-124,187,359,505,501,629/Binding site: carbohydrate (ABT)
F;36-734/Region: protein kinase ATP-binding motif
F;66-124-134/Region: protein kinase ATP-binding motif
F;66-124-134/Region: protein kinase ATP-binding site: carbohydrate (ABT)
F;30-721,122,1248/Binding site: phosphate (Tyr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
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protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 11-Jun-1999
C;Accession: A44562; A61204
R;Barcymann, C.1.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Reference number: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 CBARA
A;Residues: 1-1260 CBARA
A;Cross-references: EMBL:X03362; NID:955745; PIDN:CAA27059.1; PID:956746
R;Masui, T.; Mann, A.M.; Macacee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m 2-thiazolyJiformamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063 C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Reywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT> 1019 960 MIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVD 1019 AEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE 1079 GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY 1139 140 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1199 779 899 959 959 839 839 899 900 THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG : | :| R-KVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVWAGVGS 840 RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF 721 KANSKFIGITEL-TVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVWAGVGS RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF THOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW GAGSDVFDGDLGMGAAKGLOSLPTHDPSPLORYSEDPTVPLPSETDGVVAPLTCSPQPEY Val aB A,Accession: A61204
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 637-663, VV, 665-702 <WAS>
A,Note: authors translated the codon GCA for residue 25

E

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1077

1137 1142 1197

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EVVNQSEVQPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYL 1202
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y
Gene 140, 251-255, 1994
                                                                                                                                                                                 SEGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPPETDGYVAPLACSPQP
    CWMIDSECRERERLYSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLLEDDDMGDL
                                                                                                       VDAEEYLVPÇQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAP
                                                CWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDL
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Genetics: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID
C; Genetics: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID
C; Genetics: neu
A; Genetics: neu
C; Superfamily: epidermal growth factor receptor; protein kinase C; Keywords: ATP
F; 718-983/Domain: protein kinase homology <KIN>
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85.5%; Pred. No. 7.9e-233;
live 64; Mismatches 115; I
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F;726-734/Region: protein kinase ATP-binding motif
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Best Local Similarity 85.5'
Matches 1074; Conservative
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                                                                                        predicted
                                                (covalent)
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F;658-680/Domain: transmembrane #status predicted <TWN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;711-91,263,535,576,634/Binding site: carbohydrate (Asn) (covale: F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent)
                                                                                                                   ; Score 5843; DB 1; Length 1; Pred. No. 3.2e-233; 55; Mismatches 119; Indels
                                                                                                                     85.7%;
                                                                                                                                              Matches 1080; Conservative
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number: A00641; MUID:84219729; PMID:6328312
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A; Residues: 1-29 <ISH>
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A; Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
',798-9799,'TD',902-811,'R',813-942 <XUY>
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF recept
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.;
Science 224, 843-848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplification in A; Reference number: A43615; MUID:84196372; PMID:6326261
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A,Molecule type: protein
A,Moseidues 740-744, X', 746-747 <RUS>
A,Restidues 740-744, X', 746-747 <RUS>
R,Mosezkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A,Ttle: ATP-Stimulated interaction between epidermal growth factor receptor and superco A,Tetle: ATP-stimulated interaction between epidermal growth factor receptor and superco A,Reference number: A38023; MUID:84191554; PMID:6325948
A,Contents: annotation; receptor activity
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R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
noogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification A;Reference number: S30024; MUID:88217333; PMID:3329716
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A,Residues: 713-964 <LIN>
A,Residues: 713-964 <LIN>
A,Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley,
Biochem. Blobbyw. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
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A; Molecule type: mRNA
A; Residues: 1-1210 CULL.>
A; Residues: 1-1210 CULL.>
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
R; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A; Title: Characterization and sequence of the promoter region of the human eA; Reference number: A25772; MUID:85270438; PMID:2991899
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A; Residues: 1-29 «HAL»
A; Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A; Experimental source: carcinoma cell line A431-7
R; Xu, Y:, Ishii, S:; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.;
Nature 309, 806-810, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Mesidues: 1-29 - EHA2.
A; Residues: 1-29 - EHA2.
A; Cross-references: EMBL: X06370; NID: G31118; PIDN: CAA29668.1; PID: G31119
B; Haley, J.D.; Waterfield, M.D.
B; Biol. Chem. 266; 1146-1753, 1991
A; Title: Contributory effects of de Novo transcription and premature trans, A; Reference number: A38672; MUID: 91107677; PMID:1988448
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A; Residues: 25-30,'S',32-51;454-467 <WEB>
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Cher. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleoti
A; Reference number: A60143; MUID:85182650; PMID:298
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A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183;
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Poderical growth factor receptor precursor - human benderical growth factor receptor precursor - human NiContains: protein-tyrosine kinase (EC 2.7.1.112) erbB (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Spate: 15-Nov-1984 Heeguence revision 27-Nov-1985 #text change 11-Jun-1999 (Spate: 15-Nov-1984 Heeguence revision 27-Nov-1985 #text change 11-Jun-1999 (Spate: 15-Nov-1984) A25772; \$30024; A38672; A00642; A43615; A23062; A05281; A60143; A: FULLICH, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.; Cy. P.H. Nature 309, 418-425, 1984 Novth factor receptor cDNA sequence and aberrant expression of A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of the content

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epidermal growth factor receptor precursor - mouse
Cispecies: Mus musculus (house mouse)
Cjate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
CjAccession: A53183; A43818; S24942; A28941; S45325; 144643
R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.; I
Rémes Dev. 8, 39-413, 1994
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor ty
A;Reference number: A53183; MUID:94170986; PMID:8125255
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A;Residues: 1-1210 <LUE>
A;Cross-references: GB:U03425
R;Avivi, A; Lax, I; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.
Oncogene 6, 673-676, 1991
A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site
A;Reference number: A43818; MUID:91232866; PMID:2030916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAE 1021
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                ENNTL-VWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIP-SIATGMVGALLLLL
                                                          VVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKEQYIKAN
                                                                                                                                                 724 SKFIGITEL-TVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1082 GSDVFDGDLGNGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1199 PQGGAAPQPHFPPAFSPAFDNLYYWDQ-----DP-----PERGAPPSTFKGTPT
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R;Eisinger, D.P.; Serrero, G.
submitted to the EMBL Data Library, June 1992
A;Reference number: S24942
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A; Residues: 1-714 <AVI>
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F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predid
F;745/Active site: Lys #status experimental
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A; Conserve feetences: GDB:120610; OMIM:131550
A; Map position: 7p12.3-7p12.1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphophorylation; signal sequence #status predicted <BIG>
F; 1-24/Domain: signal sequence #status predicted <AIG>
F; 25-1210/Product: EGF receptor #status predicted <AIT>
F; 25-645/Domain: extracellular #status predicted <AIT>
F; 390-600/Domain: EGF receptor extracellular domain repeat <EE1>
F; 390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F; 4646-668/Domain: intracellular #status predicted <INT>
F; 646-668/Domain: protein kinase homology <AIN>
F; 710-975/Domain: protein kinase homology <AIN>
F; 710-975/Domain: protein kinase APP-binding motif
F; 999-1046/Region: coated-pit mediated internalization signal
                                   Ω.J.
A; Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA R; Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell 59, 33-43, 1989
A; Title: Functional independence of the epidermal growth factor receptor from a domain A; Reference number: A3331, MUID:90003233; PMID:2790960
A; Contents: annotation; internalization signal C; Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor A; Genetics:
A; Gene: GDB:EGFR
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Matches 623; Conservative 174; Mismatches 360; Indels 110;
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TYCHLY

epidermal growth factor receptor precursor - chicken

epidermal growth factor receptor precursor - chicken

N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C;Species: Gallus gallus (chicken)

C;Species: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000

C;Accession: A27720; A00643

C;Accession: A27720; A00643

C;Accession: A27720; A00643

Mol. Cell. Biol. 8, 1970-1978, 1988

A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mou A;Reference number: A27720; MUID:88261272; PMID:3260329
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A, Actesidues 1969-97. MW. 973-1318, 1988
A, Accession A2894; MUID: 88330814; PMID: 3188233
A, Accession A2894; MUID: 88330814; PMID: 318233
A, Mocession A2894; MUID: 88330814; PMID: 318233
A, Mocession A2894; MUID: 88330814; PMID: 9992, XXX, 995-996, XX, 999-1000;1002-1009, RHibbs. ML.; Dunn, A.R.; Alexander, W.S.
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44.2%; Score 3014.5; DB 1; Length 1223;
Best Local Similarity 47.9%; Pred. No. 6.2e-117;
Matches 622; Conservative 173; Mismatches 355; Indels 149;
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C,Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; Net
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/p180erbB4, a fourth member of the epidermal c
A;Reference number: A47253; MUID:93189574; PMID:8383326 1012 SPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--D 1125 1041 TPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGNFLEESIDD 1092 1126 GYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVF 1185 ----AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQ---- 1225 LTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPYWIQSGNHQ 1175 -----TAMVQNQIYNNIS 1123 655 959 714 953 773 774 833 834 893 894 895 ILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPPICTIDVYM 954 C;Species: Homo sapiens (man) C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Jun-1999 LKEQYIKANSKFIGITEL-TVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYV 774 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGM 775 MASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNWCVQIAKGM ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM IMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDD CVARCPSGVXPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV SAVV-GILL/VVLGVVFGILIKRRQQKIRKYTMRRILQETELVEPLTPSGAMPNQAQMRI AGVVGGLLCI.VVVGLGIGLYLRRR-HIVRKRTLRRLLOERELVEPLTPSGEAPNOAHLRI SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALES DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPR A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Molecule type: nucleic acid B:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360 A;Note: sequence extracted from NCBI backbone (NCBIP:126842) C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: AIP; growth factor receptor
F;716-981/Domain: protein kinase homology cKIN> ---DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1254

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1008
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                                                                                                                  NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI
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                                  Gaps
                                175;
        Length 1308
                                Indels
Score 2887.5; DB 2;
Pred. No. 1.1e-111;
...-matches 389;
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       Query Match
42.4%; Score 2887.5;
Best Local Similarity 44.5%; Pred. No. 1.1e-
Matches 599; Conservative 184; Mismatches
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A; Molecule type: DNA A; Residues: 1.1166 <WIT> A; Residues: 1.1166 <WIT> A; Cross-references: Schartl, M. Chcogene 6, 73-80, 1991 A; Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophoru: A; Reference number: S13807; WUID:91125882; PMID:1846957 A; Accession: S13809 Tu locu Roberts tyro transforming A Map position: Y
A Introns: 872/3; 888/1; 947/1; 979/3; 1025/3; 1056/1
A Introns: 872/3; 888/1; 947/1; 979/3; 1025/3; 1056/1
C Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; P; 1.25/Domain: signal sequence #status predicted <SIG>P; 25/Domain: signal sequence #status predicted <SIG>P; 25/Domain: product: kinase related transforming protein (Tu) #status predicted <MAT>P; 707-972/Domain: protein kinase homology <KIN>P; 715-723/Region: protein kinase ATP-binding motif by the melanoma-inducing 1212 -ENPFVSRR------PPKA 1198 -----FSPAFDNLYYWDQDPPERGA--PPST 1236 EDEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKÁFÖNPDÝWNHSLPPRSTLQHPDY 1258 32; GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 29 62 protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish NyAlternate names: epidermal growth factor receptor homolog; kinase-related Cispecies: Xiphophorus maculatus (southern platyfish)
Cjaceissi Xiphophorus maculatus (southern platyfish)
Cjacession: S06142; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-ind A;Reference number: S06142; MUID:90015140; PMID:2797166 PLAP-SEGAGSDVFDGDLGMGAAKGLQ | | | ::|| ::|| | ::|| XTPMSGNQFVXRDGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPV SLPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSP REGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA 4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN Gaps A;Molecule type: DNA' A;Residues: 821-1025, N',1027-1098, A',1100-1166 <ADA> A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285 C;Genetics: 142; Length 1166; Indels 38.1%; Score 2598; DB 1; Similarity 44.4%; Pred. No. 7.9e-100; 33; Conservative 167; Mismatches 397; LQEYSTKYFYKQNGRIRPIVAENPEYL 1285 A;Status: preliminary; translation not shown FKGTPT------EAPRS-Mar Local S. 563; 1056 1008 1069 1100 1116 1153 1168 1213 1199 1237 ω 9 120 Query Match Matches g ð Db 8 8 ð 셤 8 유 8 g ð g ò ò

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| YOK-NPSSPDVTQVGLKQLOLSNLTEILSGGWYSHNPLLCNVETINWWDIVDKTSNR ALTLIDTNRRRACHPCSPWCKGSRCMGBSSBDCGSLRRTVCAGGC-ACCKGDLPDCCHB TWALLIDTNRRRACHPCSPWCKGSRCMGBSSBDCGSLRRTVCAGGC-ACCKGDLPDCCHB TWALLIDTNRRRACHPCSPWCKGSRCMGBSSBDCGSLRRTVCAGGC-ACCKGDLPDCCHB COAAGCTORKABDCLACLHFMISGICELCPALVTNTDTPSBNNPBEGRYTFGASCVTA HCAGGCTGPRALDOLLACHFMISGICELCPALVTNTDTPSBNNPBEGRYTFGASCVTA HCAGGCTGPRALDOLLACHFMISGICELCAGTCCPPRALTYDTYPDTPSBNNPBEGRYTFGASCVTA THEL.PSPACKKIFGSLAFLPRSSPDGDPRARTACTPOPBOLYOPENTACTION TITL. PSPACKKIFGSLAFLPRSSPDGDPRARTACTPOPBOLYOPENTACTION TITL. STANDSCTUVCPLINNOSTOTED SANTAMANET TO THE STANDSTACTION THEL. STANDSCTUVCPLINNOSTOTED SANTAMANITYWEATOYLVINNWPB STANDSSPOKKKINGJILINRNSPEDENCGSCRACHCASCACCAGGACTAG | RLSDIYNP!<br>LTPQGGAA!<br> | PQPBYVNQPDVRPQPPSPREGPLP-AARPAGATLERAKTLSPGKNGVV |
|--|----------------------------|--|
| 123 YOK 180 ALITI 180 TMNI 239 OCPA 240 HCAC 299 CPYI 350 CPSI 351   | 1056l<br>1182 KDVI         | 5 PQP  |

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C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession. A36223; I59164
R;Kraus, M.H; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal granderne number: A36223; MUID:90083234; PMID:2687875
A;Accession: A36223
                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GB:M29366
R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J
R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-rel
A;Reference number: I59164; MUID:90311312; PMID:2164210
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A;Cross-references: GDB:119880; OMIM:190151
A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein C;Keywords: ATP; phosphotransferase
F;707-972/Domain: protein kinase homology <KIN>
F;715-723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 NADLSFLØWIKEVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVM-----LNYNT
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A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
C;Genetics:
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                                                                                                                                                        (EC 2.7.1.-) precursor
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A;Molegule type: mRNA
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EGHVTGSEAELQEKVSMCRSRSRSRSPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVN 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LPAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEYLTPQGGAAPQ 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED-----EEYEYMNRRRRHSP- 1208
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                                                                                                                                                                                                                                                                                     824
                                                                                                                                                                                                                                                                                                                                                          RRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIM 955
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                                                                                                                                                                                                                           | :: | :| : | : | : | ETELR-KLKVLGSGGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLAIG 764
                                                                                                                                                                                                                                                                                                            LEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIL 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                                                    HGVLG--AKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTV
                                                                                                                                                                               #text_change 13-Nov-1998
VFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNW
                                   SGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSA
                                                                                                                                                                  VVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
                                                                                                                                                                                                                 EQYIKANSKFIGITEL-TVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMA
                                                                                                                                                                                                                                                                           SEDHAHIVRLIGLCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYY
                                                                                                                                                                                                                                                                                                                                                                        FGKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP-SEEEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD-PSPLQRYSEDPTVPLP----SET
                      DOLFRNPHOALLHTA-NRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQFLRGQECV
                                                                     EECRVI.QGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                                                                                                                                                                              GVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor homolog precursor - rat
N;Alternate names: ErbB3 protein; HER3 protein
C;Species: Ratueus norvegicus (Norway rat)
C;Species: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 1
C;Accession: JC4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, A;Telle: Cloning of the rat ErbB3 cDNA and characterization of th A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Accession: JC43387
A;Accession: JC43387
A;Residues: 1-3,339 <HEL>
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A;Experimental source: liver
A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue .
C;Comment: This protein is a functional heregulin receptor that transduces signals to the
                                                                                           Cidentics:
A;Gene: BrbB3
C;Superfail; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologic;Superfail; unassigned Ser/Thr or Tyr-specific protein; transmembrane protein
C;Superfail; ArP; growth factor receptor; liver; phosphoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <81G>
F;1-19/Domain: signal sequence #status predicted <1MM>
F;0-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F;60-659/Domain: transmembrane #status predicted <TMM>
F;705-970/Domain: protein kinase homology <KIN>
F;713-721/Region: protein kinase APP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr) (cc
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
33.0%; Score 2246.5; DB 2; Length 1339;
Best Local Similarity 39.7%; Pred. No. 2.6e-85;
Matches 511; Conservative 173; Mismatches 441; Indels 161;
GB:U29339; NID:g915389; PID:g915390
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| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172  Qy 697 VEPLTPSGAMPNQAQMRILKEQYIKANSKFIGITEL-TVYKGIWIPDGENVKIPVAIKVL 755     | 756 RENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRG<br> | Qy 816 RLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDET 875  | Qy 876 EYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLL 935<br>    :  | OY 936 EKGERLPOPPICTIDVYMIMVKCWMIDSECRPRERELVSEPSRMARDPORFVVIO-NEDL 994 | QY 995 GPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRS 1054 | QY 1055 GCGDLTLGLEPSEERAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPL 1109 | OY 1110 ORYSEDPTVPLPSETDGYVAPLTCSPOPEYVNQPDVRPOPPSFREGPLPAARPAGATL 1167                           | QY         1168 ERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA 1212           SH         : : : : : : : : : : : : : : : : : : :   | RESULT 12 TUVUH protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H) C;Species: avian erythroblastosis virus C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999 C;Accession: A00644; A38022 | R/Yanamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. (211 35, 71-79, 1983) A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene famil A;Reference number: A00644; MUID:84026539; PMID:6313229 | A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 1-604 <xam> A;Residues: 03.</xam></xam></xam></xam></xam></xam></xam>  | A;Residues: 1-28, W, 30-139,'F',141-145,'V',147-152 <deb> A;Residues: 1-28,W',30-139,'F',141-145,'V',147-152 <deb> A;Cross-references: GB:K02006 C;Genetics: A;Gene: erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;130-395/Domain: protein kinase homology <kin> F;138-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted</kin></deb></deb> |
|---|--|--|---|---|--|--|---|---|---|---|--|---|
| Db 758 MLAVGSLDHAHIVRLLGELCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIA 817  Qy 831 KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA 890 | 891 LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 950 | Qy 951 VYMIMYKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASFLDSTFYRSLLE 1010 | QY         1011 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE 1068           1   1   1   1   1   1   1   1   1   1 | OY 1069EAPRSPLAPSEGAGSDVPDGDLGMGAAKGLQSLP 1102                          | Oy 1103 THDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQ 1142                    | OY 1143 PDVRPQPPSPREGPLPAARPAGATLERAKTLSP-GKNGVVKDV 1184    :        | Qy         1185 FAFGGAVENPEYLTPOGGAAPQPHPP 1210           Db         1192ERYEYMURKRRGSP-PRPP 1209 | RESULT 11  TVFVLV  protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase C;Species: avian leukosis virus, ALV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun:1999 C;Arcession: ROMA43. | ; Raines, M<br>sing and pro   | 18763 1; PID:9211750<br>designated as Gallus gal<br>1.  | Jane: 939-517-10-120.  Superfamily: epidermal growth factor receptor; protein kinase homology  (eywords: ATP: oncogene; phosphotransferase; transforming protein; tyrosine-specific preference: agg protein (fragment) #status predicted <gags. #status="" (fragment)="" 194-459="" 202-210="" 229="" 7-59="" 80-698="" <erbs="" <ern's="" <kin's="" active="" atp-binding="" domain:="" env="" erbb="" homology="" kinase="" lys="" motif="" predicted="" predicted<="" product:="" protein="" protein-tyrosine="" region:="" site:="" td=""><td>Ouery Match Best Local Similarity 50.8%; Pred. No. 1.4e-62; Matches 364; Conservative 80; Mismatches 146; Indels 127; Gaps 20;  Qy 578 GPEADQCVACAHYKDPPFCVARCPSGVKDDLSYMPIWKPDEEGACQPCPINCTHSCVDL 637                                       </td></gags.> | Ouery Match Best Local Similarity 50.8%; Pred. No. 1.4e-62; Matches 364; Conservative 80; Mismatches 146; Indels 127; Gaps 20;  Qy 578 GPEADQCVACAHYKDPPFCVARCPSGVKDDLSYMPIWKPDEEGACQPCPINCTHSCVDL 637  |

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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus
C;Species: avian erythroblastosis virus
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C;Sacession: S35745
R;Vennatroem, B.
Submitted to the EMBL Data Library, March 1993
A;Reference number: S35743
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A;Residues: 1-544 <vUN>
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                                           18;
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                                             Gaps
                                           128;
  Length 604;
23.8%; Score 1623; DB 1; Length 6. 50.7%; Pred. No. 5.1e-60; ive 76; Mismatches 137; Indels
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C;Accession: S00727
R;Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.
Rocogene Res. 1, 265-278, 1987
A;Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutant A;Reference number: S00727; MUID:88217326; PMID:2897102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055 GGGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPL 1109
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                                                                                                    RLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDET
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                                                                            GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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                                      Gaps
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                                      94;
Length 544;
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                                      Indels
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5; DB 2;
4.4e-58;
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  Score 1575;
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53.4%;
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                    Best Local Similarity
Matches 336; Conserv
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A; Residues: 1-545 <SCO>
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Length 545;

Score 1568; DB 2; Pred. No. 8.5e-58;

23.0%; 53.4%; 13

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| 120   IKANSKFIGITEL-TVYKGIMIPDGENVKIPVAIKULRENTSPRANKEILDEAYVMAGVG 778   1: |            |            |            | 4"       | . 2   | 0 9  | н го  | Н 44    | 80 M                        |                            |  |
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| 720 IKANSKFIGITEL-TVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYW  11.            | 778<br>868 | 838<br>928 | 895<br>984 | 955      | 101   |  | 112   | 118     | 121                         |                            |  |
|   |            |            |            |          | VKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDS       :   : | DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHRHRSSTRSGGGDLTLGLEPS | PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSED |         | KDVFAFGGAVENPEYLTPQGGAAPQPH | NLYYWD<br>:     <br>HEYYND |  |
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Search completed: July 22, 2003, 09:27:50 Job time: 30.2855 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 22, 2003, 09:10:23; Search time 22.179 Seconds (without alignments) 5413.772 Million cell updates/sec

SEQ4-710-730-12 6775

Title: Perfect score:

1 MELAALCRWGLLLALLPPGA.......TFKGTPTAENPEYLGLDVPV 1249 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | æ              |        |     | SUMMARIES |                    |
|---------------|--------|----------------|--------|-----|-----------|--------------------|
| Result<br>No. | Score  | Query<br>Match | Length | DB  | ID        | Description        |
| -             | 6602   | 97.4           | 1255   | . ⊣ | A24571    | protein-tyrosine k |
| 7             | 5805   | 85.7           | 1260   | Н   | TVRTNU    | protein-tyrosine k |
| ٣             | 5795.5 | 85.5           | 1254   | 7   | 148161    | p-185 precursor -  |
| 4             | 3030   | 44.7           | 1210   | Н   | GQHUE     | epidermal growth f |
| S             | 3001   | 44.3           | 1210   | N   | A53183    |                    |
| 9             | 2978.5 | 44.0           | 1223   | Н   | TVCHLV    |                    |
| 7             | 2849.5 | 42.1           | 1308   | 7   | A47253    |                    |
| 80            | 2553   | 37.7           | 1166   | ٦   | S06142    | >                  |
| 6             | 2305.5 | 34.0           | 1342   | ~   | A36223    | kinase-related tra |
| 10            | 2218.5 | 32.7           | 1339   | ~   | JC4387    | epidermal growth f |
| 11            | 1650.5 | 24.4           | 698    | Н   | TVFVLV    | ~                  |
| 12            | 1588   | 23.4           | 604    | ٦   | TVYUH     | protein-tyrosine k |
| 13            | 1537   | 22.7           | 544    | 7   | S35745    | protein-tyrosine k |
| 14            | 1530   | 22.6           | 545    | 7   | 800727    | kinase-related tra |
| 15            | 1523.5 | 22.5           | 1330   | Н   | GOFFE     | epidermal growth f |
| 16            | 1513   | 22.3           | 540    | N   | B44776    |                    |
| 17            | 1511   | 22.3           | 540    |     | TVFVEB    | yrosin             |
| 18            | 1509   | 22.3           | 644    | N   | A36325    | epidermal growth f |
| 19            | 1224   | 18.1           | 1323   |     | E88257    | et-23              |
| . 20          | 1224   | 18.1           | 1374   |     | 870712    | protein-tyrosine k |
| 21            | 1139   | 16.8           | 1369   | ~   | S70713    | protein-tyrosine k |
| 22            | 1126   | 16.6           | 527    |     | A42032    |                    |
| 23            | 1109   | 16.4           |        | Н   | A45558    |                    |
| 24            | 975.5  | 14.4           | 843    |     | A27131    | epidermal growth f |
| 25            | 806.5  | 11.9           | 346    | N   | S13807    | >                  |
| 26            | 754.5  | 11.1           | 311    | ~   | S13808    | protein-tyrosine k |
| 27            | 703    | 10.4           | 1363   | ď   | T43220    | insulin-like growt |
| 28            | 676.5  | 10.0           | 1372   | ~   | A34157    | recep              |
| 29            | 675    | 10.0           | 1382   | ٦   | INHUR     | insulin receptor p |

| insulin receptor p | insulin receptor-r | protein-tyrosine k | insulin-like growt | insulin receptor-r | insulin-like growt | insulin-like growt | protein-tyrosine k | protein-tyrosine k | insulin receptor - | protein-tyrosine k | insulin receptor ( | protein-tyrosine k | insulin receptor - | mouse developmenta | eph-related recept |
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| A36080             | A36502             | T18534             | T43212             | B36502             | IGHUR1             | A33837             | A54092             | 805582             | A56081             | 150612             | S57245             | A39753             | T30346             | I48652             | 148953             |
| ~                  | ~                  | ~                  | N                  | ~                  | Н                  | 7                  | ~                  | Н                  | Н                  | 7                  | N                  | 7                  | ~                  | ~                  | ~                  |
| 1383               | 1300               | 1477               | 1607               | 1268               | 1367               | 1371               | 987                | 1114               | 2148               | 952                | 2101               | 984                | 1390               | 987                | 987                |
| 6.6                | 9.5                | 9.5                | 9.4                | 9.3                | 9.0                | 8.7                | 9.8                | 9.8                | 9.8                | 8.5                | 8.5                | 8.4                | 8.4                | 8.4                | 8.2                |
| 4                  | 3.5                | 643                | 634                | 632                | 607                | 588                | 586                | 583                | 579.5              | 574.5              | 573                | 571.5              | 568                | 266                | 555.5              |
| 67                 | 64                 |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

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| SS |   |

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB;

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text\_change 11-Jun-1999
C; Accession: A24571; A25:491; A4188; B44188; I59509; I57622
R; Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; 7 Nature 319, 230-234, 1986
A; Yattele: Similarity A24571; MUID: 86118663; PMID: 3003577
A; Reference number: A24571; MUID: 86118663; PMID: 3003577

A; Accession: A24571

A; Molecule type: mRNA A; Mesdidues: 1-1255 < YAM. A; Cross-references: GB.Xv. A; Cross-references: GB.Xv. R; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Neull. Acad. Sci. U. S.A. 82, 6497 -6501, 1985 A; Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm? A; Reference number: A25491; MUID:86016729; PMID:2995967

Accession: A25491

A;Molecule type: DNA A;Residues: 737-1031 <SEM> A;Cross-references: 781-1031 <SEM> A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P Scance 230, 1132-1139, 1985 A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosc A;Reference number: A44188; MUID:86070181; PMID:2999974

A;Accession: A44188 A;Molecule type: DNA A;Residues: 740-910 <COUI> A;Cross.references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

Molecule type: mRNA

A;Residues: 1.5pc: M.RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Residues: 1.5pc: M.H.'; RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: 159509; MUID:85272597; PMID:2992089
A;Accession: 159509

Status: translated from GB/EMBL/DDBJ

A; Residues: 832-909 <REX.
A; Residues: 832-909 <REX.
A; Residues: 832-909 <REX.
A; Risidues: Ri

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA

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A,Accession: A61204
A,Status: preliminary
A,Molecule type: DNA
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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAAS8637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3G
GGenetics
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Gross-references: GDB:120613; OMIM:164870
A;Map position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
                                                                                                                                                                                                          inase
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: extracellular #status predicted <EXT>
F.22-653/Domain: extracellular #status predicted <EXT>
F.70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F.70-305/Domain: intracellular domain repeat <EE2>
F.654-675/Domain: intracellular #status predicted <IVM>
F.664-255/Domain: intracellular #status predicted <IVM>
F.718-983/Domain: protein kinase homology <KIN>
F.718-983/Domain: protein kinase AFP-binding motif
F.66/1255/Domain: protein kinase AFP-binding motif
F.66/124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.68/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F.753/Active site: Lys #status predicted
F.139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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Pred. No. 3.2e-277;
6; Mismatches 21; Indels
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A;Title: The new oncogene encodes an epidermal growth factor receptor-related protein. A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Recente number: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 CBARA
A;Residues: 1-1260 CBARA
A;Cross-references: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B;Masul, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, A;Title: Direct DNA sequencing of the rat new oncogene transmembrane domain reveals no mto 2-thiazolyljformamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063 C;Superfamily: epidermal growth factor receptor; protein kinase homology Kreywords Arto-rate and autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphot F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT> 1133 1019 1079 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVPAFGGAVENPEYLTP 1193 VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1199 MIDSECRPRERELVSEFSRMARDPORFVVIONEDLGPASPLDSTFYRSLLEDDDMGDLVD 1013 AEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE 1073 779 953 720 773 833 839 893 THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW 959 9 protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 11-Jun-1999 C;Accession: A21562; A6120 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL RKVKVLGSGAFGTVYKGIWIPDGENVK-IPVAIKVLRENTSPKANKEILDEAVVMAGVGS RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF THQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYM1MVKCW GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY 1080 GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL RKVKVLGSGAFGQYIKA-----NSKFIGITELVLRENTSPKANKEILDEAYVMAGVGS PYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV Val aB A;Residues: 637-663,'V',665-702 <MAS>
A;Note: authors translated the codon GCA for residue 25 C;Genetics:

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p-185 precursor - golden hamster (5) Species: Mesocricetus auratus (golden hamster) C;Species: Mesocricetus auratus (golden hamster) C;Species: O2-Jul-1996 #text_change 18-Jun-1999 C;Accession: 140161 R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; I Shakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; I Gene 140, 251-255, 1994 A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene. A;Reference number: 148161 MUID: 94193007; PMID: 7908275 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1254 RES> A;Cross-references: GB:D16295; NID:q493236; PIDN:BAA03801.1; PID:g747595 C;Genetics: A;Gene: neu C;Staperfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP F;18-983/Domain: protein kinase homology KIN> F;726-734/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                EYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1191
                                                                                                                          VDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                                                                                                                                                                                                                   1203 VPREGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAENPEYLGLDVPV 1260
                                                                          SEGAGSDVFD\SDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPPETDGYVAPLACSPQP
   VDAEEYLVPQQQFFSPDPTPGTGSTAHRRHRSSSTRSGGGELTLGLEPSEEGPPRSPLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELTYLPANATLSFLQDIQEVQGYMLIAHSQVRHVPLQRLRIVRGTQLFEDKYALAVLDNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDL
                                                                                                                                                                                             SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MELAALCRWGLILALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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85.2%; Pred. No. 1.7e-242;
ive 62; Mismatches 115; Indels 9;
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Best Local Similarity 85.2
Matches 1070; Conservative
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F;658-680,Domain: transmembrane #status predicted <TWN>
F;723-988/Domain: protein kinase homology <KIN>
F;723-739/Fegion: protein kinase APP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #statu
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;788/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
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                                                                                                                                                                         10;
                                                                                                                                                                         53; Mismatches 119; Indels
                                                                                                                                        Score 5805; DB 1;
Pred. No. 6.8e-243;
                                                                                                                                        85.7%;
85.5%;
                                                                                                                                                        Best Local Similarity 85.5
Matches 1076, Conservative
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Y.; Ishikawa,

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Gaps

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120 180 180 240 240 300

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A;Residues: 1-1210 "CULL>
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
Frishii, S.; Xu, Y.; Stratton, H.; Roce, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal groval Reference number: A25772; MUID:85270438; PMID:2991899
                                                                                                                                                                                                                                           A, Molecule type: DNA
A, Residues: 1.29 <16H>
A, Residues: 1.29 <16H>
A, Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
A, Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
B, Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
A, Flales, J.; 375-396; 1987
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A;Title: Contributory effects of de Novo transcription and premature transcript terminata.
A;Reference number: A38672; MUID:91107677; PMID:1988448
number: A00641; MUID:84219729; PMID:6328312
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A;Status: translation not shown
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A; Residues: 1-29 <HA2>
                                          A; Molecule type: mRNA
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A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197,'A', 199-222,'S', 224-304,'RA', 307-321,'
',798-799,'TD', 802-811,'R', 813-942 < xUY.
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF recept
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.A
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Xiu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Mex Nature 309, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs A; Reference number: A00642; MUID:84245835; PMID:6330563
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A;Residues: 740-744, 'X', 746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
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A;Title: ATP-stimulated interaction between epidermal growth factor receptor and A;Reference number: A38023; MUID:84191554; PMID:6325948
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                                                                              A;Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
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A;Residues: 713-964 <LIN>
A;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F:A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter,
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
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A;Molecule Lype: mRNA
A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
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A;Reference number: A05281; MUID:84172183; PMID:6324343
A;Accession: A05281
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A; Residues: 25-30, 'S', 32-51,454-467 < WEB>
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros,
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A; Title: Identification of residues in the nucl
A; Reference number: A60143; MUID:85182650; PMID
A; Molecule type: DNA
A; Residues: 1-29 <HAL>
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Nature 309, 418-425, 1984
A,Tlitle: Human epidermal growth factor receptor cDNA sequence and aberrant expression of
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Spidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 1.5.Nov-1984 #sequence revision 27.Nov-1985 #text change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43515; A23062; A05281; A60143; A33
R;Ullrich; A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.; Y
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A; Contents: annotation; receptor activity

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Cypeciaes: Mus musculus (house mouse)
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Ryluetteke, N. Cy; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.; I Genes Dev. 8, 399-413, 1994
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor ty A; Reference number: A53183; MUID:94170986; PMID:812525
A;Accession: A53183
A;Molecule type: mRNA
A;Reference number: A53183; MUID:94170986; PMID:812525
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A;Accession: A43818
A;Molecule type: mRNA
A;Residues: 1-714 <AVIx
A;Cross-references: GB:X59698
R;Esinger, D.P.; Serrero, G.
Submitted to the EMBL Data Library, June 1992
A;Reference number: S24942
A;Accession: S24942
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A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA B;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell S9, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain rate from number: A3331; MUID:9000323; PMID:279050
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor C;Genetics:
A;Gene: GBB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
A;Gene: GBB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
A;Map position: 7pl2.3-7pl2.1
C;Genetics:
C;Genetics:
C;Genetics:
A;Gene: GB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
A;Gene: GB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
A;Gene: GB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
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A;Cross-references: GBB:120610; OMIM:131550
A;Gene: GB:EGFR
A;Cross-references: GBB:120610; OMIM:131550
A;Map position: Telefrence #status predicted <a href="Mailto-26">MAILTO-26">MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILTO-26"/MAILT
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Matches 618; Conservative 175; Mismatches 357; Indels 118;
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48.7%; Pred. No. 2.2e-123;
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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: dallus gallus (chicken)
C;Dace: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
R;Lax, I: Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstrr
Mol. Call siol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mousine A;Reference number: A27720; MUID:88261272; PMID:3260329
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                       123 SVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
                                                                         DOLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE
                                                                                           ECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPS
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Pijermal growth factor raceptor, HER4 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.; Foy, L.; Net
Proc. Natl. Acad. Sci. US;A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4(p)80exbB4, a fourth member of the epidermal g
A;Reference number: A47253; MUID:93189574; PMID:8383326
A;Accession: A4723
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic &cid
A;Molecule type: nucleic &cid
A;Molecule type: nucleic &cid
A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     954 MIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERWHLPSPTDSKFYRTLMEE 1013
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                                                                                                                                                       CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
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                                                                                                                                                                                                                                                                       LKETELRKVKVLGSGAFGQ----YIKANSKF---IGITELVLRENTSPKANKEILDEAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKG
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A; Accession: A27720
A; Molecule type: mRNA
A; Residues: 1-123 < LAX>
A; Residues: 1-123 < LAX>
A; Cross-references: GB:M20386
B; Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and procession: A00643; MUID:8522822; PMID:2988784
A; Reference number: A00643; MUID:8522822; PMID:2988784
A; Rocession: A00643
A; Residues: 585-1223 < NIL>
A; Residues: 585-1223 < NIL>
A; Cross-references: GB:M10066
A; Cross-references: GB:M10066
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C; Genetics:
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P:1-30/Domain: signal sequence #status predicted <SIG>
P:1-31/Domain: signal sequence #status predicted <SIG>
P:1-1223/Product: epidermal growth factor receptor #status predicted <MAT>
P:31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
P:31-654/Domain: extracellular #status predicted <MAT>
P:31-650/Domain: EGF receptor extracellular domain repeat <EE1>
P:397-610/Domain: EGF receptor extracellular domain repeat <EE2>
P:597-610/Domain: protein #status predicted <INM>
P:597-610/Domain: protein kinase homology <KIN>
P:719-394/Domain: protein kinase ATP-binding motif
P:719-394/Domain: protein kinase ATP-binding motif
P:719-50/Binding site: carbohydrate (Ser) (covalent) #status predicted
P:136.202.280.361,370,422,575,580.615,635/Binding site: carbohydrate (Ser) (covalent) #status predicted
P:697/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
P:754/Active site: Lys #status predicted
P:100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #sta
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44.0%; Score 2978.5; DB 1;
Best Local Similarity 47.5%; Pred. No. 3.6e-121;
Matches 618; Conservative 173; Mismatches 352;
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| . 59;   | 64   | 67<br>124   | 127           | 184  | 243  | 303  | 297  | 363<br>355   | 423   | 48  | 475 | 543<br>535   | 602  | 651 | 652              | 710<br>708   | 764  | 768 | 824  | 884  | 944 | 948 | 1003   |  |
| ch<br>1 Similarity 44.1%; Score 2849.5; DB 2; Length 1308;<br>593; Conservative 184; Mismatches 390; Indels 179; Gaps | WGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYOGCOVVQGNLELTY | WWWSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEITS<br>LPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN |               | NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI<br> | DINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGG-ARCKGPLPTDCCHEQCAAG | CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY | CSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNF | LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE | PAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQUVFETLEEITGYLYI SAWPDSLPDLS | VPQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRSCLALIHHNTHLCFVHTVPWD |     | OLFRNPHQALLHTANRPEDECVGEGLACHOLCARGHCWQPGPTQCVNCSQFLRGQBCVEE | CRVLQGLPREYVNARHCLPCHPECQP-ONGSVTCFGPEADQCVACAHYKDPPFCVARCPS |     |                  | TSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQA   :  :  :  :  : | OMRILKETELRKVKVLGSGAFGOYIKANSKFIGIŢELVLRENTSPKANKEILDE |     | AYWAGYGSPYVSRLGICLTSTVQLYTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA   :   :   : | KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA |     |     | VYMINVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNED-LGPASPLDSTFYRSLL | EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE |
| ដូច   | σ (  | 8 5   | 89            | 125  | 185  | 244  | 238  | 304<br>298   | 364   | 424   | 416 | 484  | 544  | 603 | 596              | 652<br>653   | 711  | 709 | 765  | 825  | 885 | 889 | 945  | 1004   |
| Query Ma<br>Best Loc<br>Matches   | à á  | g &   | QQ            | <b>상</b> 원   | දු පු  | č  | g  | & a  | & a   | 'n  | ф   | & 8<br>8   | . 40   | ð í | අ <sub>ධ</sub> , | <u>8</u> &   | ò  | g   | දු පු  | රු සි  | ò   | qq  | <u>&amp;</u> &   | l à  |

Nilternate names: epidermal growth factor receptor homolog; kinase-related transforming C; Species: Xiphophorus maculatus (southern platyfish)
C; Species: Xiphophorus maculatus (southern platyfish)
C; Species: Xiphophorus maculatus (southern platyfish)
C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000
C; Accession: S06142; S13809
R; Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Robertsc Nature 341, 415-81, 1380
A; Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu loculary putative receptor tyrosine kinase encoded by the melanoma-inducing Tu loculary A; Testerence number: S06142; MUID: 90015140; PMID: 2797166
A; Residues: 1-1166 <WIT>
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A; Reference number: S0807; WID: 91125882; PMID: 1846957
A; Reference number: S13809
A; Reference number: S13809
A; Reference number: preliminary; translation not shown A;Gene: mrk
A;Map position: Y
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A;Matcons: 872/3; 998/1; 947/1; 979/3; 1025/3; 1056/1
C;Maywords: 872/3; epidermal growth factor receptor; phosphotransferase; transmembrane protein; tyros: C;Maywords: AfP; growth factor receptor; phosphotransferase; transmembrane protein; F;1-25/Domain: signal sequence #status predicted <SIG>F;2-25/Domain: signal sequence #status predicted <MAT>F;707-972/Domain: protein kinase homology <KIN>F;715-723/Region: protein kinase AFP-binding motif 1009 DEEDLEDMMDAEEYLVP-QAFNIPPP-----IYTSRARIDSNRS-----EIGHSPPPAY 1056 1206 | | | | ::|| ::|| | ::|| | | | ::|| | 116 --PLAP-SEGAGSDVFDGDLGMGAAKGLQS 1094 1095 LPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR 1147 1168 ENPFVSRR------PPKAE 1199 1200 DEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKÁFÖNPDÝWNHSLPPRSTLQHPDYL 1259 ----FSPAFDNLYYWDQDPPERGA--PPSTF 1231 31; 119 120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIPHKNNQL 179 29 62 1148 EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA-4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 8 AALLQ--LLLVLSISRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNVVLEN 60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN Indels 146; Gaps A;Status: preliminary; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 821-1025 'N',1027-1098,'A',1100-1166 <ADA> A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285 C;Genetics: Length 1166; Query Match 37.7%; Score 2553; DB 1; Sest Local Similarity 43.9%; Pred. No. 7.3e-103; Matches 557; Conservative 166; Mismatches 399; 1260 QEYSTKYFYKQNGRIRPIVAENPEYL 1285 1232 KGTPT----1064 APRS-1207 ò 유 ò g ò 셤 ò q ò 셤 ò 셤 ò

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| 3 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWMDIVDKTSNP 179 0 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238 | 239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESWPNPEGRYTFGASCVTA 298 | 9 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358 | 9 ITEL-BEAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLOVFETLEEITGYLYISAWPD 417   : | 8 SLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 ::                   : | 7 VHTVPWDQLFRNPHQALLHTANRPEDBECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 536 | 7 GOECVEECRVLOGLPREYNNARHCLPCHPECOPQNGSVTCFGPEADQCVACAHYKDPPFC 596 | 7 VARCESGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEGRASPLTSIVS 656 | 7 AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK 716<br> | 7 ETELRKVKVLGSGAFGQYIKANSKFIGITELVLRENTSPKANKEILDEAYVMAG 770 | 1 VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLANWCMQIAKGMSYL 830 | 1 EDVRIVHRDLAARNVIVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR 890<br> - | 1 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMINV 950 | 1 KCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD 1010 | LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSST<br>         <br>VVDADEYLLPYKRI | PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ<br> | 0 QPEYVNQPDVRPQPPSPREGPLP-AARPAGATLERAKTLSPGKNGVVK 1176 | DVFAFCGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPT 123 |
|---|--|--|--|---|---|--|--|--|--|---|--|--|---|---|--|---|--|
| ,123 YC<br>180 AI<br>180 Th   | 239 QC<br>240 HC   | 299 CE<br>300 CE   | 359 II<br> <br>357 SI  | 418 SI<br>::<br>417 NN  | 477 VF:<br>:<br>477 AN  | 537 GC<br> -<br>529 GC   | 597 VP<br>:<br>589 II  | 657 AV<br> <br> <br>  647 LV   | 717 ET<br>  <br>   | 771 VG  | 831 ED<br>  :<br>  826 EE  | 891 RE<br>886 WT   | 951 KC<br>     <br>946 KC   | 1011 EV<br>1001 UV  | 1071 PS                                | 1130 QF<br>1056   | 1177 DV  |
| op<br>Oy<br>Oy  | Sp. og.  | \$ 9a  | <b>상</b> 임   | දුරු පු   | <i>&amp;</i> 8  | è 9  | δ <b>α</b>   | رن<br>و<br>و   | <u>ئ</u> ۾   | රු අු   | රු සි  | <b>상</b> 임   | & 8<br>8  | <u>ئ</u> ۾  | දු පු                                  | <u>\$</u> 8   | è a  |

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C;Accession: A36223; Es9164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal gn A;Accession: A36223; MUID: 90083234; PMID: 2687875
A;Accession: A36223; MUID: 90083234; PMID: 2687875
A;Accession: A36223; MUID: 90083234; PMID: 2687875
A;Accession: A36223; MUID: 90083234; PMID: 2687875
A;Accession: A36223; MUID: 90083234; PMID: 2687875
A;Accession: A342 acka.
A;Accession: A;Accession: U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-rel
A;Reference number: 159164
A;Reference number: 159164
A;Residues: 1-559, G', 561-957, F', 959-1063, G', 1065-1342 acks
A;Residues: 1-559, G', 561-957, F', 959-1063, G', 1065-1342 acks
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A;Gene: GDB: ERBB3; HER3
A;Gene: GDB: ERBB3; HER3
A;Gene: GDB: ERBB3; HER3
A;Gene: GDB: ERBB3; HER3
A;Gene: GDB: ERBB3; HER3
A;Gene: GDB: ERBB3; HER3
A;Cross-references: GBB: 119880; OMIM: 190151
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C; Keywords: ATP: phomalin: protein kinase homology c; Reywords: ATP: phomalin: protein kinase homology F;707-972/Begion: protein kinase homology city
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 DQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPKACEGTG-----SGSRRQTVDSSNIDG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKF--IGITELE- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTKILGNLDFLITGLNGDPWHKIPALDPEKLNVFRTVREITGYLNIQSWPPHMHNFS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 NADLSFLOWIREVTGYVLVAMNEFSTLPEPNLRVVRGTQVYDGKFAIFVM----LNYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GLILALIPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 NASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT
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3 LAALCRWGLLLALLPPGAA---STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN LQVLC----FLLSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE

62

298 289

QCAAGCTGPKHSDCLACLHFNHSG1CELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA

CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGL--GMQYIKANSKF

416 403 475 463

ID----GFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVREITGYLNIQSWP

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A,Cross-references: GB:U29339; NID:g915389, PID:g915390
A,Experimental source: liver
A,Note: law authors translated the codon AAC for residue 369 as Thr and GTT for residue.
C,Comment: This protein is a functional heregulin receptor that transduces signals to the C,Genetics:
C,Genetics:
A,Gene: ErbB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.7%; Score 2218.5; DB 2; Length 1339; Best Local Similarity 39.6%; Pred. No. 2.1e-88; Matches 509; Conservative 168; Mismatches 443; Indels 165;
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                                                                                                                                   EECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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                                                                                   DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
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476 FVHTVPWDQLFRNPHQALLHTA-NRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQF
                                    YHHSINWTRLIRGPSEERLDIKYDRPLGECLAEGKVCDPLCSSGGCWGPAPGQCLSCRNY
                                                                                                                    LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                                                         524 SREGVCVTHCNFLQGEPREFVHEAQCFSCHPECLPMEGTSTYNGSGSDACARCAHFRDGP
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                                                                                                                                                                                                                                                                                             584 HCVNSCPHGILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLMSKPH
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| qq   | 759 LAVGSLDHAHIVRLIGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIAK 818   | qq  | 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172   |
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| ç,<br>Dp   | 826 GMSYLEDVRLVHRDLAARNYLVKSPNHVK.TDFGLARLLDIDETEYHADGGKVPIKMMAL 885<br>   | ò qa  | 697 VEPLTPSGAMPNOAQMRILKETELRKVKVLGSGAFQ0YIKANSKFIGITELV 748  |
| & a  | 886 ESILRRFTHQSDVMSYGVTVWELWTFGAKPYDGIPAREIPDLLEKGERLEQPPICTIDV 945  | QV<br>ab  | 749 IRENTSPKANKEILDEAYVMAGVGSPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENR 808<br>  |
| දු පු  | 946 YMINVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLED 1005  | oy<br>op  | 809 GRLGSQDLLAWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDE 868<br>  |
| <u>ک</u> ۾   | 1006 DDMGDLVDABEXLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE 1062 1:   | ςς<br>Q   | 869 TEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIFAREIPDL 928<br>     -  |
| Sp GS  | 1063EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT 1097 1022 TSLGSALSLPTGTLTRPRGSQSLLSPSSGYMPMNQSSLGEACLDSAVLGGREQFSRPISL 1081  | රු අ  | 929 LEKGERLPQPFICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NED 987  |
| oy<br>Dp   | 1098 HDPSPLQRYSEDPTVPLPSETDGXVAPLSPQPEYVNQP 1137 1082 H-PIPRGRPASESSEGHVTGSEAELQEKVSVCRSRSRSRSPRPRGDSAYHSQR 1133   | S S   | 988 LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTR 1047<br>:                         411 MHLPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFFNSPST- 513   |
| SP GS  | 1138 DVRPQPPSPREGPLPAARPAGATLERAKTLSP-GKNGVVKDVF 1179 1134 HSLLTPVTPLSPPGLEEEDGNGYVMPDTHLRGASSSREGTLSSVGLSSVLGTEEEDED 1191   | çy<br>Pp  | 1048 SGGGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSP 1102   |
| oy<br>Op   | 1180 AFGGAVENPEYLTPQGGAAPQPHPP 1204<br>          : :        <br>1192EEYEYMNRKRGSP-PRPP 1209  | Qy<br>Dp  | 1103 LQRYSEDPTVPLPSETDGYVAPLTCSPQPEYUNQPDVRPQPPSPREGPLPAARPAGAT 1160<br>  |
| RESULT<br>TVFVLV<br>Protein<br>N; Conta<br>C; Speci<br>C; Date:                | tyrosine kinase<br>un-1999   | 6 % B %   | 1161 LERAKTLSPGKNGVVKDVF  |
| Cell 4:<br>Cell 4:<br>A; Titl(<br>A; Refer<br>A; Acces                         | dun, b.b.; Kalines, M  | RESULT<br>TVYUH<br>protein<br>C;Speci   | 12<br>1-tyrosine kinase (3C 2.7.1.112) erbB - avian erythroblastosis virus (strain H)<br>es: avian erythroblastosis virus<br>18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999  |
| A; Resid<br>A; Crost<br>A; Note<br>C; Comme<br>C; Genet                        | .1; PID:g211750<br>gnated as Gallus gal  | C;Acces<br>R;Yamam<br>Cell 35<br>A;Title<br>A;Refer   | sion: A00644; A38022<br>loto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.<br>, 71-78, 1983<br>. The erbB gene of avian erythroblastosis virus is a member of the src gene family<br>ence number: A00644; MUID:84026539; PMID:6313229   |
| A; Gene<br>C; Supe:<br>C; Keyw<br>F; 1-6/1<br>F; 7-59/<br>F; 194-4<br>F; 202-2 | A;Gene: gag-env-erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;1-6/Product: gag protein (fragment) #status predicted <gag> F;7-59/Product: env protein (fragment) #status predicted <env> F;0-698/Product: protein-tyrosine kinase erbB #status predicted <erb> F;194-459/Domain: protein kinase homology <kin> F;202-210/Region: protein kinase ATP-binding motif F;229/Active site: Lys #status predicted</kin></erb></env></gag> | A, Mcces<br>A, Molec<br>A, Resid<br>A, Cross<br>R, Debui<br>Science<br>A, Title<br>A, Refer<br>A, Refer | A;Accession: A00644 A;Accession: A00644 A;Mesidues: L-6Cule type: DNA A;Residues: L-6Cule type: DNA A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678 A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678 B;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, E Science 224, 1456-1459, 1984 A;Itle: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of c A;Reference number: A38022; MUID:84223957; PMID:6328658 A;Accession: A38022 |
| Quer<br>Best<br>Match  | Gaps 21;   | A; Molec<br>A; Resid<br>A; Cross<br>C; Genet  | ule type: DNA<br>.uss: 1-28,'W', 30-159,'F',141-145,'V',147-152 <deb><br/>.treferences: GB:KO2006<br/>ics.</deb>  |
| oy de s  | 637  | A; General C; Super C; Super C; Keywo F; 130-3  | einys<br>rdainys epidermal growth factor receptor; protein kinase homology<br>rdas: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific py<br>95/Domain: protein kinase homology «KIN»<br>46/Region: protein kinase ATP-binding motif  |
| ò  | 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVVLGVVFGILIKRRQQK.RKYTMRRLLQETEL 696<br>:   | F;165/A   | ctive site: Lys #status predicted   |

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AjGene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Reywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
C;Reywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;135-400/Domain: protein kinase ATP-binding motif
F;130/Active site: Lys #status predicted
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535745
Fig. 19
535745
Cypecies: avian erythroblastosis virus
Cypecies: avian erythroblastosis virus
Cypecies: avian erythroblastosis virus
Cypecies: avian erythroblastosis virus
Cypecies: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997
Cypecossion: S35745
Submitted to the EMBL Data Library, March 1993
A;Reference number: S35743
A;Accession: S35745
A;Accession: S35745
A;Accession: S35745
A;Cose-references: EMBL:X12707
C;Genetics:
                                                                                  RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                    Gaps
23.4%; Score 1588; DB 1; Length 604; 50.1%; Pred. No. 1.4e-61; ive 75; Mismatches 134; Indels 136;
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                   Similarity
                  Best Local Sim
Matches 347;
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kinger-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus (1 Species: avian erythroblastosis virus C; Species: avian erythroblastosis virus C; Species: 01-Dec.1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C; Accession: S00727 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C; Accession: S00727 #s. 56-278, 1987 A; Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutants A; Reference number: S00727; MUID:88217326; PMID:2897102 A; Molecule type: DNA A; Residues: 1-545 <SCO> A; Coss-references: EMBL:X06943 C; Genetics:
                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .050 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1105 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1163
                                                                            637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE 353
                                                                                                                                                                                                                                                                                                                                                174 EATSPKANKEILDEAYVWASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PVREDGFL----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISK 523
                                                                            578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                  VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGQYIK-----ANSKFIGITELVLR
                                                                                                                                                                                                                                                      638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                          ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
                                        Gaps
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                                        98;
  Length 544;
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                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Mismatches 131;
, DB 2;
2e-59;
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Pred. No. 3.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: erbB
C,Superfamily: epidermal growth factor receptor; px
C,Keywords: ATP; phosphotransferase
F;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1164 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1191
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22.7%; Score 1537; 52.5%; Pred. No. 2e
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52.5%;
                Best_Local Similarity 52.59
Matches 330; Conservative
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Best Local Similarity
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| Matches* 330; Conservative 68; Mismatches 132; Indels 98; Gaps 16;   | A, Cross-references: FlyBase: FBgn0003731   |
|--|---|
|  | A,Map position: 2 57F   |
|  | C;Superramily: epidermal growth ractor receptor; protein kinase homology C;Cycyords: ATP; autophosphorylation; duplication; plycoprotein; phosphot P: 733,700ms; correctly attached and action and action and action.   |
| •  | F;1-/32/DOMain: extracellular #status predicted <exi><br/>F;733-764/Domain: transmembrane #status predicted <tmm></tmm></exi>   |
| 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETEL   | F;765-1330/Domain: intracellular #status predicted <int><br/>F;808-1072/Domain: protein kinase homology <kin></kin></int>   |
| Db 58 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 113  | F;816-824/Region: protein kinase ATP-binding motif<br>F:122.300.324.363.518.686.695.700/Binding site: carbobydrate (Asn) (covalent) #status pre   |
| Qy       697 VEPLTPSGAMPNQAQMRILKETELRKVKULGSGAPGQYIKANSKPIGITELVLR 750         IIII   | F;774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;843/Active site: Lys #status predicted F;81181/Binding site: phosphate (Tvr) (covalent) (by sutophosphorylarion) #status predicted   |
| RVITS DK ANKETT I INDA KIVA GEOVICE I I I I I I I I I I I I I I I I I I  | A THE COLUMN THE CONTRACT OF THE COLUMN THE |
|  | QUELY MACCH. S. 23.53; SOCIE 122.33; DB 1; DENGUL 1330; BEST LOCAL SIMilarity 28.88; Pred. No. 1.8e-58; Matches 400; Conservative 178; Mismatches 416; Indels 393; Gaps 43;   |
| Qy 811 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 870  | 3YVLIAHNCVROVPLORLRIVRGTOLFEDNYALAVLDNGDPLNNTTPV  |
| 234 IGSQYLLNWCVQIAKGMYLEERHLVHRDLAARNULVKTPQDVKITDFGLAKQLGADEKE  | 38 ITNYIVIGEDLIPCTLSYRLOIIRGRTLFSILSVEEEKYALFVTY  |
|  | יייי אפיטיאיים די זין איז איז איז איז איז איז איז איז איז איז   |
| 294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMIFGSKPYDGIPASEISSVLE   | OY 135 GOLKELDGARSHILDINGGVILDGARSTOLITHANDIFHANNULALLILDINGSACHF 194  DD 82 SKMYTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQMSEIVSNGTDAYYNYDFTAPERECPK 141   |
| QY 931 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQ-NEDLG 989  | Qy 195 CSPMCKGSRCWGESSEDÇQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDC 252   |
| DD 354 KGERLPQPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMH 413  | Db 142 CHESCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGFKPRECCHLFCAGGCTGFTQKDC 200   |
| QY 990 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1049   | VTYNTDTFESMPN   |
| Db 414 LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFFNSPST 454   | Db 201 IACKNFFDEAVSKEBCPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACV 259   |
| PLAPSEGAG  | Qy 313 LVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELEFAG 366   |
| :     :  | Db 260 RSCPQDKWDKGGECVPCNGPCPKTCPGVTVLHAGNIDSFRN 300  |
| 1105 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRQPPSPREGPLPAARPAGAT-LER   | 367 CKKIFGSLAFLPESFDGDPASNTAPLOPEQLOVETLEEITGXLYISAWPDS   |
| DD 482PVREDGFLPAPEYVNQLMPKKPSTAMVQNQIYNYISLTAISK 523   | Db 301 CTVIDGNIRILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKEITGYLNIEGTHPQ 360   |
| Qy         1164 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1191           Db         524 LPMDSRYQNSHSTAVDNPEYL 544   | Qy 419 LPDLSVPQNLQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFV 477 :    -          :    :    :    :    :   |
|  | 478 HTVPWDQLFRNPHQALLHTANRPEDEC   |
|  | Db 421 SNIRWPAIQKEPEQKVWVNENLRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSV 480   |
| epidermal growth factor receptor - fruit fly (Drosophila melanogaster)<br>NyContains: protein-tyrosine kinase (BC 2.7.1.112) erbB  | Qy 505 504  |
| C.brettes: Diosophila metalogaster<br>C.brete: 17-Mar-1997 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999<br>C.bression: Mondan, Nobols   | Db 481 QRGRLLGSWHG3VPYLQELQFQWHLHRRLWLYIQVSINSTQDKSNEHQLTDACYSFSVPT 540   |
| Ribivneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.   | δγ 505γG 506  |
| A.Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding A:Reference number: A0640. MITD.85124611. DMTD.382469  | Db 541 SLTIERARYAIQSAGLAMELEQITARSASMRHSKTLPAEGRQVPRWVFLGVCASARAGIA 600   |
| A; Accession: A00640   | FLRG  |
| Aprolectie type: DNA Aprolecti | Db 601 BPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCETECPADHYTDEE 654   |
| Ajirobs relectances: Embi:NO3054<br>R:Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.<br>Nature 314 178-180 1888  | KDPPFCV   |
| A.Title: A brosophila genomic sequence with homology to human epidermal growth factor re<br>A.Reference number: A38021: MITD:85137918: PMTD:9681332  | Db 655 QRECFQRHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTSKCPLE 708   |
| A; Accession: A38021   | LDDKGCPAEQRASPLTS   |
| A:Residues: 'A',832-866,'V',868-943,'QTPSLVK' <wad><br/>A:Cross-references: EMR:X0293: NTD:G7922: PIDN:CAA26157 1: DID:G93956</wad>  | Db 709 MRHVNYQYTAIGPYCAASPPRSSKITANLDVMMIFIITGAV 749  |
| C;Comment: This sequence is tentative because the introns have not been identified. C;Genetics:  | FGI -LIKRRQQKIRKYT MRRLLQETELVEPLTPSGAMPNQA   |
| Ger (  | Db 750 LVPICILCVVTYICRQKQKAKKETVKWTMALSGREDSEPLRPSNIGANLCKLRIVKDAE 809  |

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949 MVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLG--PASPLDSTFYRSLLEDD 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1136 MPKLNRYCKDPSNKNSSTGDDERDSSAREVGVGNLR---------LDL 1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1064 AP-----RSPLAPSEGAGSDVFDG---DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL 1114
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                                                                                                                                                                                                                                                                                                                                                                       832 DVRLVHRDLAARNVLVK---SPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESI 888
                                                               772 GSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLE 831
                                                                                                                                                                                                                                                  868 EHVNLLKILAVCMSSQMMLITQLMPLGCLLDYVRNNRDKIGSKALLNWSTQIAKGMSYLE 927
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720 LRKVKVLGSGAFGQYIKA-----NSKF-IGITELVLRENTSPKANKEILDEAYVMAGV 771
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1273 DHEYYND 1279
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Search completed: July 22, 2003, 09:28:04 Job time : 27.179 secs

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OM protein - protein search, using sw model

July 22, 2003, 08:47:04; Search time 10.5911 Seconds (without alignments) 4891.279 Million cell updates/sec Run on:

SEQ4-710-730-12 6775 1 MELAALCRWGLLIALLPPGA.....TFKGTPTAENPEYLGLDVPV 1249 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Length DB ID Descri | . 4 1255 1 RRB2 HIMAN | .8 1257 1 ERB2_RAT P06494 ratti | .5 1254 1 ERB2_MESAU Q60553 1 | .7 1210 1 EGFR_HUMAN P00533 | .3 1210 1 EGFR_MOUSE Q01279 mus m | .1 1308 | .8 1308 1 ERB4_RAT Q62956 | .9 1167 1 XMRK_XIPMA P13388 | .2 1342 1 ERB3_HUMAN P21860 | .1 1339 1 ERB3_RAT Q62799 | .2 1426 1 EGFR_DROME P04412 | .1 634 1 ERBB_ALV P00534 | .5 703 1 EGFR_CHICK P1338 | .4 604 1 ERBE_AVIER P00535 avian e | .4 540 1 ERBE_AVIEU P11273 avian | .1 1323 1 LT23_CAEEL | .9 245 1 ERB2_MOUSE P70424 1 | .4 1363 1 ILPR_BRALA | .0 1372 1 | .9 1383 1 INSR_RAT | .9 1382 1 INSR_HUMAN | .7 1300 1 IRR_MOUSE Q9wt14 mus m | .6 1297 1 IRR_HUMAN P1 | .5 1300 1 IRR_CAVPO P14617 cavia | .5 1477 1 HTK7_HYDAT Q25197 hydra | .4 1607 1 MIPR_LYMST Q25410 lymna | .0 1367 1 IG1R HUMAN P08069 | .7 1373 1 IGIR_MOUSE Q60751 mus m | .6 987 1 EPB4_HUMAN P5476 | .6 1370 1 IGIR_RAT P24062 rattu | .6 1114 1 RET_HUMAN P07949 | .5 984 1 EPB1 CHICK 007494 |
|-----------|---------------------|-----------------------|---------------------------------|-------------------------------|-----------------------------|-----------------------------------|---------|---------------------------|-----------------------------|-----------------------------|---------------------------|-----------------------------|--------------------------|---------------------------|------------------------------------|----------------------------------|----------------------|------------------------------|----------------------|-----------|--------------------|----------------------|----------------------------------|------------------------|----------------------------------|-----------------------------------|-----------------------------------|-----------------------------|-----------------------------------|---------------------------|---------------------------------|----------------------------|----------------------------|
|           | Length              | · m                   | S                               | ~                             | 1210                        | 1210                              | 1308    | 1308                      | 1167                        | 1342                        | 1339                      | 1426                        | 634                      | 703                       | 604                                | 540                              | 1323                 | 245                          | m                    | 1372      | 1383               | 1382                 | 1300                             | 1297                   | 1300                             | 1477                              | 1607                              | 36                          | 1373                              | 987                       | 1370                            | 1114                       | 984                        |
| de        | Query<br>Match      | 97.4                  | 'n                              | 5                             | •                           | 44.3                              |         | ä                         | ۲.                          | 4.                          | ë.                        | 7.                          | 4.                       | 23.5                      | ٠.<br>د                            | ٠.                               | æ                    |                              |                      |           |                    | 9.9                  | •                                | •                      | •                                | •                                 | ٠                                 | •                           | •                                 |                           |                                 |                            | 8                          |
|           | Score               | 6602                  | 5811                            | 5795.5                        | 3028                        | 3002                              | 2849.5  | 2830                      | 26                          | 2314.5                      | 24                        | Н                           | 1633.5                   | 1595                      | 1588                               | 1520                             | _                    | 1142.5                       | 703                  | 676.5     | 674                | 673                  | 629                              |                        | 644.5                            | 643                               | 634                               | 607                         | 589                               | 586                       | 585.5                           |                            | 574.5                      |
|           | Result<br>No.       | -                     | . ~                             | ٣                             | 4                           | 2                                 | 9       | 7                         | 80                          | σ                           | 10                        | 11                          |                          | 13                        |                                    | 15                               | 16                   | 17                           | 18                   | 19        | 20                 | 21                   | 22                               | 23                     | 24                               | 25                                | 26                                | 27                          | 28                                | 29                        | 30                              | 31                         | 32                         |

| P09759 rattus norv | 093105 aedes aegyp | P54761 mus musculu | P54762 homo sapien | 091736 xenopus lae | Q91571 xenopus lae | Q03145 mus musculu | P29317 homo sapien | Q91694 xenopus lae | P54753 homo sapien | Q91845 xenopus lae | P18460 gallus gall |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
| EPB1 RAT           | INSR_AEDAE         | EPB4 MOUSE         | EPB1 HUMAN         | EPBB_XENLA         | EPBA_XENLA         | EPA2 MOUSE         | EPA2 HUMAN         | EP4B XENLA         | EPB3 HUMAN         | EP4A XENLA         | CEK2_CHICK         |
| -                  | ;<br>⊣             | _                  | _<br>_             | -                  | _                  | Н                  | _                  | -                  | _                  | -                  | -                  |
| 984                | 1390               | 987                | 984                | 902                | 985                | 716                | 976                | 985                | 966                | 986                | 908                |
| 8.4                | 8.4                | 8.4                | 8.3                | 8.3                | 8.1                | 8.1                | 7.9                | 7.9                | 7.9                | 7.9                | 7.9                |
| 571.5              | 268                | 266                | 565.5              | 559                | 551.5              | 547.5              | 538.5              | 535.5              | 535                | 534.5              | 534                |
| 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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301 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; 1848/U;

InterPro; IPR000199; EGFR L domain.

R InterPro; IPR000174; FurIn-like.

DR InterPro; IPR00174; FurIn-like.

DR InterPro; IPR001245; TYL_Pkinase.

DR InterPro; IPR001245; TYL_Pkinase.

BR InterPro; IPR004019; YLP_motif.

DR Pfam; PF00769; pkinase; I.

DR Pfam; PF00757; YLP; Z.

DR Pfam; PF00101; Euk_pkinase; I.

DR Pfam; PF00101; Euk_pkinase; I.

R SMART; SM00219; TYKC; I.

R SMART; SM00219; TYKC; I.

R PROSITE; PS00110; PROTEIN KINASE ATP; I.

R PROSITE; PS00119; PROTEIN KINASE DOM; I.

W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; TAUNAL SIGNAL.

TAUNAL STONAL I.

TAUNAL I.

TAUNAL I.

POTENTIAL.

TAUNAL I.

POTENTIAL.
PTM: LIGAND-BINDING INCREASES PHOSPHOKIDALLON ON TREED BREIDUES (BY SIMILARITY).

RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE FOURS ALLELES DUE TO THE VARIATIONS IN POSTTIONS 654 AND 655. ALLELE B1 (654-LIE-LIE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-LIE-VAL-655) HAS A FREQUENCY OF 0.782; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE SEE PROPERTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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EMBL; M11761; AAA35808.1; JOINED.
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11764; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11766; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; JOINED.
EMBL; M11730; AAA35808.1; -..
EMBL; M2036; AAA35978.1; -..
EMBL; X0336; CAA27060.1; -...
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PIR; A24571; A24571.
HSSP; P11362; 1FGK.
Genew; HGNC:3430; ERBB2.
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                                                                                                                                                    MIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVD 1013
                 THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW 959
                                         PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV 833
                                                                            RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF 893
                                                                                                                THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW 953
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                                                    721 RKVKVLGSGAFGQYIKA-----NSKFIGITELVLRENTSPKANKEILDEAYVMAGVGS
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MEDLINE=86118662; PubMed=3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UTN-2002 (Rel. 37, Last annotation update)
Receptor protein-tyrosine kinase erbs-2 precursor (EC 2.7.1.112)
(p188crb82) (NEU protein chase erbs-2) (Epidermal growth factor receptor-related protein).
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MEDLINE=92155181; PubMed=1346763;
Gullick W.J.; Bottomley A.C., Lofts F.J., Doak D.G., Mulvey
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Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase
expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 852-905 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 319:226-230(1986)
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Newman R., Crumpton N.J., Sternberg M.J.E., Campbell I.D.; "Three dimensional structure of the transmembrane region of the proto-oncogenic and oncogenic forms of the neu protein.";
                                                                                                        ALTHOUGHT NEUREGULING DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPPOR. NOT ACTIVATED BY EGF. TGF-ALPHA AND AMPHIREGULIN:

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.
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EXTRACELLULAR (POTENTIAL).
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Transferase, Tyrosine-protein kinase, ATP-binding, Phosphorylation,
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-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR001249; EM& Prinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YIP motif.
Pfam; PF00069; pkinase; I.
Pfam; PF00130; Recep L domain; 2.
Pfam; PF01030; Recep L domain; 2.
ProDom; PD000001; Eu; pkinase; 1.
SWART; SW00261; FU; 3.
SWART; SW00261; FU; 3.
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|   | RESULT 3  REREA MESAU STANDARD; PRT; 1254 AA.  1D — REREA MESAU STANDARD; PRT; 1254 AA.  1D 16-DEC-1998 (Rel. 37, Last sequence update)  DT 15-DEC-1998 (Rel. 37, Last sequence update)  DT 15-DEC-1998 (Rel. 37, Last sequence update)  DT 15-DEC-1998 (Rel. 37, Last sequence update)  DE RECEDOR POCOLAIN LAST ANDOCATION PUDDATES DE PRESENCE (BC 2.7.1.112)  DE RESEDOR NEUL  OS MESOCTICEUS auratus (Golden hamster).  OC MESOCTICEUS  ON NEUL  OC MESOCTICEUS  ON NEUL  OC MESOCTICEUS  ON NEUL | CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial |
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1014 AEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE 1073
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RR HSP; P11362, 1FGK.
InterPro; IPR000199; EUK_pkinase.
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R InterPro; IPR001245; Try_pkinase.
R InterPro; IPR001034; Eurin-like; 1.
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R ROSITE; PS01010; PROTEIN KINASE DOM; 1.
Transmembrane; GlycoproteIn; Multigene family; Receptor; Signal; M Transferase; Tyrosine-Protein; Multigene family; R-Tansmembrane; Disease mutation; M Proto-oncogene; Disease muta
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entities requires a license agreement ( or send an email to license@isb-sib.ch)
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Ullixioh A., Coussens L., Hayfilck J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
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expression of the amplified gene in A431 epidermoid carcinoma cells.";
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                                                  1194 QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1249
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                                                                                                                                    EGFR HUMAN STANDARD; PRT; 1210 AA.
P00531; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732;
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01-NOV-1997 (Rel. 35, Last sequence update)
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RA 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor.";
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MEDLINE=21100872; Pubmed=11161793;
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MEDLINE=8817333; PubMed=3329716;
Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich
Waterfield M.D.;
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MEDLINE=85270438; PubMed=2991899;
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MEDLINE=91107677; PubMed=1988448;
Haley J.D., Waterfield M.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=98225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
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-!- FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.

-!- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                      atypical
                                                               Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.; "Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster ovary fibroblasts.";
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  ASN-175; ASN-413; ASN-444 AND
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ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/
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Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.;
"Characterization of the N-oligosaccharides attached to the atyy
Asn-X-Cys sequence of recombinant human epidermal growth factor
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Pred. No. 5.6e-155;
1; Mismatches 358; Indels 118;
                                                                                                                                                                                              CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568
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CARBOHYDRATE-LINKAGE SITES ASN-128;
                                          MEDLINE=96398132; PubMed=8962717;
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                                                                                                                                                     Growth Factors 13:121-132(1996).
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EMBL; U48726; AAC50798.1; -.
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LILALIPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN

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74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNMYYENSYALAVLSNYD
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 ----APSRDPHYQD--PHSTAVGNPEYLN 1140
                                           1192 TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTFKGTP 1235
                                                           TVQ------PTCVNSTFDSPAHWAQKGSHQISLDNPDVQQDFFPKEAKPNGIFKGS- 1190
1133 YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL- 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisinger D.P., Serrero G., Supply GenBank/DDBJ databases.
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GF30 AND
VACCINIA VIRUS GROWTH FATOR (BY SIMILARITY).
-!- CATALATIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIM-BALB/C, and CD-1; TISSUE-Liver, and Decidua;
STRAIM-BALB/C, and CD-1; TISSUE-Liver, and Decidua;
MEDLINE-93126380; PubMed-7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
"Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE STAIN=BALD/c; TISSUB=Liver;
MEDLINE=93026370; Pubmed=1408137;
Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94170986; PubMed=8125255; Letteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S., Jenkins N.A., Lee D.C.; "The mouse waved-2 phenotype results from a point mutation in the receptor tyrosine kinase.";
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                          2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC
                                                                                                                                                                    PRT; 1210 AA
                   YINO-SVPKRPAGSVONPVYHNOPLNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 969-1117 FROM N.A.
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STRAIN=BALB/c, TISSUE=Liver;
Hibbs M.L.;
                                                                                                                                                                                                                                                                                                                                                          (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-714 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes Dev. 8:399-413(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding site.";
Oncogene 6:673-676(1991)
                                                                                                                                                                    STANDARD;
                                                                                      1236 TAENPEYL 1243
                                                                                                           1191 TAENAEYL 1198
                                                                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Q01279;
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MIDSECRPRERVSEPSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLV 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NSPST-----SRTPLLSS 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQ 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1040 LSATSN----NSTVACINRNGSCRVKEDAFLORYSSDPTGAVTEDNIDDAFL----PV 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNTAQ-----PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFKG 1189
  RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF
                                                                                                                                                                                                                                                                                                                                                                            THQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCW
                                                                     PYVSRLLGICTISTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
                                                                                                                                                                                                                                                          THOSDVWSYG'/TVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEYVNQPDVRFQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
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tissue distribution and differential processing in response to
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T5-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (BC 2.7.1.112)
(p180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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TISSUE=breast carcinoma;
MEDLINE=31.85 to Pubmed=383326;
Plowman G.D., Cullouscou J.-M., Whitney G.S., Green J.M., Carlto
Poy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER4/p180erbB4, a fourth member
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1308 AA
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J. Biol. Chem. 272:26761-26768(1997)
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MEDLINE=97476287; PubMed=9334263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721
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(BY SIMILARITY).
(BY SIMILARITY).
MAJOR SITE)
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llarity 48.6%; Pred. No. 1.4e-153;
Conservative 168; Mismatches 365; Indels
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                                                                                              tyrosine phosphate.

-!- SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBE
RECEPTORS (POTENTIAL).

-!- SUBCELLULAR LOCATION: TYPE I membrane protein.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;

ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CERBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.

-!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CERBBELLUM, PITUTARY, SPLEEN, TESTIS AND BREAST: LOWER LEVELS IN THYMUS, LUNG, SALLYARY GLAND, AND PANCHEAS.

-- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR InterPro; IPRO00494; EGFR L domain.

InterPro; IPRO00719; Euk pkinase.

BR InterPro; IPRO00719; Fukinase.

BR InterPro; IPRO001245; Tyr pkinase.

DR InterPro; IPRO01245; Tyr pkinase.

BR Propor; Prof0075; Furin-like; 1.

BR Propor; Prof0075; Recep_L_domain; 2.

BR Propor; Prof0075; Fukin-like; 1.

BR PROF15; SM00261; Fuk pkinase; 1.

BR SMART; SM00261; Fuk pkinase; 1.

BR SMART; SM00219; TyrKc; 1.

BR SMART; SM00219; TyrKc; 1.

BR SMART; SM00109; PROTEIN KINASE ATP; 1.

R PROSITE; PSC00119; PROTEIN KINASE DOM; 1.

W Transmembrane; Glycoprotein; Multiqene family; Receptor; Signal; Transmembrane; Glycoprotein; Multiqene family; Phosphorylation; Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation; Transmembrane; Such States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States and States a
                   2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN. CATIVATED BY EGF. TGF-A, ADD AMPHIREGULIN. CATIVITY: ATP + a protein tyrosine = ADP + protein
  FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                     --IAAGVIGGLFILVIVGLTFAVYVRRKSIK-KKRALRRFL-ETELVEPLTPSGTAPNQA 708
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536 CNLYDGEFREFENGSICVECDPQCEKMEDGLL/TCHGPGPDNCTKCSHFKDGPNCVEKCPD 595
                                      596 GLOGANSF -- IFKYADPDRECHPCHPNCTOGCNGPTSHDCIYYPWTGHSTLPQHAR-TPL 652
                                                                                                                                          AYVWAGVGSPYVSRILGICLTSTVQLVTQLMPYGCILDHVRENRGRLGSQDLLNWCMQIA 824
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                                                                                                               TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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                    GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC------PAEQRASPL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERB4_RAT STANDARD; PRT; 1308 AA. 626256; 0922XN; 15-05C-1998 (Rel. 37, Created) 15-JW-2002 (Rel. 41, Last sequence update) 15-JW-2002 (Rel. 41, Last annotation update) Receptor protein-tyrosine kinase erbB-4 precursor ERBB4 OR TYRO-2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTORS (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extended family of protein-tyrosine kinase genes differentially
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SMART; SM00219; TYrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
TRANSMEMBY PROTEIN KINASE TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                            "Neuregulins promote survival and growth of cardiac myocytes. Persistence of ErbB2 and ErbB4 expression in neonatal and adult ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
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InterPro; IPR000195; Euk pkinase.
InterPro; IPR001245; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; Tyr pkinase.
InterPro; IPR004019; Tyr pkinase.
Ffam; PF00757; Furin-like; 1.
Ffam; PF01010; Recep L domain; 2.
Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010; Recep L domain; 3.
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Pfam; PF01010; Recep L domain; 3.
Pfam; PF01010010; Recep L domain; 3.
Pfam; PF01010010; Recep L domain; 3.
Pfa
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Lai C., Lemke G.;
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EMBL; U52531; AAC53051.1; -.
HSSP; P11362; 1FGK.
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SEQUENCE OF 848-901 FROM N.A.
Marchionni M.A., Kelly R.A.;
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| P. DOWALN   196   334   CYS-RICH.   F. DOWALN   456   633   CYS-RICH.   CYS- | Qy 7 297 TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKF 356  291 KKCPHNFV-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTV 348 |

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1167 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                   Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.
01-JAN-1990 (Rel. 13, Created)
LoCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41. Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
                                                                                                                                                                                                         MEDLINE=90015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Telling A., Robertson S.M., Schartl M.;
Novel putative receptor tyrosine kinase encoded by the melanoma-
inducing Tu locus in Xiphophorus.";
Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBCELULAR LOCATION: Type I membrane protein.
-!- DISBASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE BGF RECEPTOR FAMILY.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
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Xiphophorus maculatus (Southern platyfish)
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HSSP; P11362; 1FGK.
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Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.
  KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD 1010
                                                                                                                                                                                                                                                                          LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1070
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AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK 716
                                         ETELRKVKVLGSGAFGQYIK----ANSKFIGITELVLRENTSPKANKEILDEAYVMAG 770
                                                                                 VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL 830
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                                                                                                                                                              891 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV 950
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(c-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=90083234; PubMed=2687875;
Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.;
"Isolation and characterization of ERBB3, a third member of the
ERBB/epidermal growth factor receptor family: evidence for
overexpression in a subset of human mammary tumors.";
Proc. Natl. Acad. Sci. U.S.A. 86:9191-9197(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT PORM).

- ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SHZ OR SH3 DOWAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

- PTW: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PRS. SUBUNIT OF PHOSPHATIDYLINGSTOL. SASOCIATION AND SIMILARITY.

- DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KINASE ERBB-3
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SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                     expression of an additional epidermal growth
                                                                                                                                                                                                                         MEDLINE-9328282; PubMed=7685162;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor
tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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ATP (BY SIMILARITY)..
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Todaro G.J., Shoyab M.;
Molecular cloning and expression of an addition.
factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
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InterPro; IPR000174; Euk pkinase.
InterPro; IPR001245; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00030; Recep L domain; 2.
ProDom; PD000001; Euk pkinase; 1.
                                                                                                                                                                  FROM N.A. (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M29366; AAA35790.1; -. EMBL; M34309; AAA35879.1; -. EMBL; S61953, AAB26935.1; -. PIR; A36223; A5223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew, HGNC:3431; ERBB3.
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SIGNAL 1 1
CHAIN 20 134
                                                                                                                                                                                                 TISSUE=Placenta;
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| Qy 483 DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV 541 :: |  | Qy 602 SGVKPDLSYMPIWKFPDEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA 657 | Qy 658 VVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILK 716 | Qy 717 ETELRKVKVLGSGAFGQYIKANSKFIGITELVLRENTSPKANKEILDEAYVMAG 770                           | Qy 771 VGSPYVSELLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL 830 : ::   | Qy 831 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR 890 | Qy 891 RRFTHQSDVWSYGVTVWELMTFGARPYDGIPAREIPDLLEKGERLPQPPICTIDVYMINV 950 :: | Oy 951 KCWMIDSECRPRPRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1007   | Qy 1008 MGDLVDABEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP-SEEEAPR 1066  :  | Qy 1067 SPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD-PSPLQRYSEDPTVPLPSETD 1119  | Qy 1120 GYVA PLTCSPQPEYVNQPDVRPQPPSPREGP 1150                | Qy 1151LPAARPAGATLERAKTLSP-GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQP 1201 | Qy 1202 HPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYL 1243              | 50 M   | Q6ZP9; Q6ZP5;<br>15-DEC-1998 (Rel. 37, Created)<br>15-JUN-2002 (Rel. 41, Last sequence update)<br>15-JUN-2002 (Rel. 41, Last annotation update) | receptor protein-tyrobine kind (c-ebb3). ERBB3. Rattus norvegicus (Rat). | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. OX NCBI_TaxID=10116; RN [1] RP SEQUENCE FROM N.A. |
|--|--|--|---|---|--|---|--|---|---|--|--|--|--|--|---|--|---|
| 210 218 BY S<br>214 226 BY S<br>227 235 BY S                               | 231 243 BY<br>246 255 BY<br>259 286 BY<br>290 301 BY | 305 320 BY S<br>323 327 BY S<br>500 509 BY S<br>504 517 BY S       | 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                   | 5/6 585 BY SIMILARITY. 5/8 610 BY SIMILARITY. 613 621 BY SIMILARITY. 617 629 BY SIMILARITY. | 120 N-LINKED (GLCNAC ) ( 353 353 N-LINKED (GLCNAC ) ( 408 408 N-LINKED (GLCNAC ) ( 408 N-LINKED | 437 437 N-LINKED (GLUNAC  | 183 BILSGGVYIEKNDKLCHMDTIDWR<br>183 SC -> GOFPMVEGLTPQPADW                 | VANSPLIC 184 1342 MISSING (IN SHORT ISOFORM).  CONFLICT 560 560 E -> G (IN REF. 2).  CONFLICT 1064 1064 E -> G (IN REF. 2).  SEQUENCE 1342 AA; 148097 MW; 7201E7F66CA374BD CRC64; | <pre>ery Match 34.2%; Score 2314.5; DB 1; Length 1342; st Local Similarity 39.6%; Pred. No. 1.1e-116; cches 520; Conservative 191; Mismatches 462; Indels 141; Gaps 35;</pre> | 10 GLILALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67  11 GLLESLARGSEVGNSQAVCPGTLNGLSVTGDAENOYOTIYKI,YERCEVVAGNLETYTGT 70 | NASLSFLQDIOEVOGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT | LALTLIDIN<br>:: :<br>AEIVVKD                                     | 188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG 246 | 247 PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST 306  :: | 307 DVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYGLGWQYIKANSKFIGITELE- 363  | 364 FAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDSLPDLS 423     | 424 VFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW 482<br>  |

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595 FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDKGCPAEQRASPLT 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLIDIAR LOCATION: Type I membrane protein.
-!- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-!- FTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3. EXTRACELLULAR (POTENTIAL).
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Pfam; PF00069; pkinase; 1.
Pfam; PF00157; Furin-like; 1.
Pfam; PF00109; Turin-like; 1.
PRINTS; PR00109; TYRKINASE; 1.
SMART; SM00261; FU; 5.
SMART; SM00261; FU; 5.
PROSITE; PS00109; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Glycoprotein, Multigene family; Receptor; Signal;
Transferase; Tyrosine_protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                            MEDLINE=96096535; PubMed=8522190; Hellyer N.J. Koland J.G.; Hellyer N.J. Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.; "Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein."; Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                    REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
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|  | Query Match<br>Best Local<br>Matches 51   |  | Φ ¥   | , ZH   | 12.    | 18   | 23 23  | 29   | 29    | 35.   | 34.   | 417   | 47  | 46,   | m  | 52.2                                      | 595  |
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YMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLED 1005
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                                                                                                                                                                                                                                                                    SIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQ 711
                                      712 MRILKETELRKVKVLGSGAFGQYIK-----ANSKFIGITELVLRENTSPKANKEILDEA 765
                                                                            GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMAL 885
                                                                                                                                                                          ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV 945
                                                                                                766 YVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQLAK
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C P044I2; 061601; 09W2G0; P81868;
T 13-AUG-1987 (Rel. 05, Created)
T 13-DEC-1998 (Rel. 37, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Bidermal growth factor receptor precursor (BC 2.7.1.112) (Egfr.)
E Gutkern receptor) (Torpedo protein) (Drosophila relative of BRBB).
E GERR OR TOP OR C-ERBB OR DER OR C10079.
S Drosophila melanogaster (Fruit fly).
C Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
C Bukaryota; Metazoa; Neoptera; Endopterygota; Diptera; Brachycera;
C Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular analysis of the Drosophila EGF receptor homolog reveals that several genetically defined classes of alleles cluster in subdomains of the receptor protein."; Genetics 137:531-550(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II).
MEDLINE=94350209; Pubmed=8070664;
Clifford R., Schupbach T.;
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REVIEW

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100 KICIGTKSRLSVPSNKEHHYRNLRDRYTNCTYVDGNLKLTWLPNENLDLSFLDNIREVTG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITEL-----EFAGCKK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PODKMDKGGE----CVPCNGPCPKTC------PGVTVLHAGNIDSFRNCTV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 KNFFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 IFGSLAFLPESFDG--DPASNTA-----PLOPEQLOVFETLEEITGYLYISAWPDSLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 IDGNIRILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKEITGYLNIEGTHPQFRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing; Developmental protein.
SIGNAL 1 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 456; Conservative 183; Mismatches 433; Indels 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1845; DB 1; Length 1426;
Pred, No. 1.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIDERMAL GROWTH FACTOR R
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Receptor; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
             PIR; A00640; GQFFE.
HSSP, P11362; IFGK.
FlyBase; FB901000731; Egfr.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR00019; Euk Dkinase.
InterPro; IPR00119; Furin-like.
InterPro; IPR001245; Tyr Dkinase.
                                                                                                        domain
                                                                                                                                                                                                                                                                                                                PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                              domain; 2,
                                                                                                                                                                                                        Pfam, PF00069, pkinase, I.
Pfam, PF00075, Furin-like, 1.
Pfam, PF01030, Recep L domain
PRINTS, PR00109, TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.2%;
                                                                                                                                                                                                                                                                                                              ProDom, PD000001, Euk pki)
SMART, SM00261, FU, 7.
SMART, SM00219, TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
NP_BIND
BINDING
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   BGF receptor.";

Cell 89:13-16 (1997)

LEUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAP-MAPK PATHWAY. INVOLVED IN A WYRIAD OF DEVELOPMENTAL DECISIONS.
CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE COCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.
INSUES SPECIFICITY: UBIQUITYOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOCEMETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECUENCE THIS PATTERN IS REPRESSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND
                                                                        SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                      Perrimon N., Perkins L.A.; "There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                  ANALYSIS.
MEDLINE-92038942; PubMed=1936959;
Raz E., Schejter E.D., Shilo B.S.;
"Interallelic complementation among DER/fib alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases."; Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF052754; AAC08536.1; -.
EMBL, AF052753; AAC08536.1; JOINED.
EMBL, AF052754; AAC08535.1; -.
EMBL, AF052752; AAC08535.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF109078; AAD26133.1; -. AF109084; AAD26133.1; JOINED.
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AF109079; AAD26131.1; JOINED.
AF109083; AAD26131.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD26132.1; JOINED.
                                                                                                                                                                                                                                                                                                           WEDLINE=97248481; PubMed=9094709;
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K03417; AAA51460.1; -.
K03418; AAA50965.1; -.
K03418; AAA51461.1; -.
AF109077; AAD26132.1; -.
AF109078; AAD26132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE003454; AAF46732.1; -.
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growth factor receptor.";
Nature 314:178-180(1985).
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45;

Phosphorylation; Transferase;

RECEPTOR

82

315

322

255

263

602

540

482

421

EMBL;

EMBL; EMBL; EMBL;

EMBL;

EMBL; EMBI,; EMBL;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

EMBL;

EMBL; EMBL;

EMBL;

RNA

novel

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-!-- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- MISCELLANBOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIRAL PROMOURER ELEMBNITS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
-!- MISCELLANBOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
            MEDLINE=85228222; PubMed=2988784;
Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbB activation in ALV-induced erythroblastosis: nov
processing and promoter insertion result in expression
amino-truncated EGF receptor.";
Cell 41:719-726(1985).
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SEQUENCE
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                                                                                                                                                                                                                                                                                        1241 AKPDDYLOPKAAPGPS-----HKTDCT-------DEMPKLNRYCKDPSNKN 1279
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                                                                                                                                                                                              843
---PDI 608
                                                           713
                                                                                                | | :: | |: | |- | GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCET 771
                                                                                                                                                                                                                                                   YICROKOKAKKETVKMTMALSGCEDSEPLRPSNIGANLCKLRİVKDAELRKGGVLGMGAF 949
                                                                                                                                                                                                                                                                           GQYIKA-----NSKF-IGITELVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGIC 783
                                                                                                                                                                                                                                                                                                                                                                                                                      VTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRF 963
                                                                                                                                                      772 ECPADHYTDEEQRECFQRHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTS 831
                                                                                                                                                                                                                                                                                                                                                                       NVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYG 903
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                                                                                                                                   ----SC----NDLDDKG---
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                                   P---SGVK---
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                                                                                 SYMPIWKF - - PDEEGACQP-
                                                                                                                                                                               -CPAEOR-----
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                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 MPNQAQMRILKETELRKVKVLGSGAFGQ----YIKANSKF---IGITELVLRENTSPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 APNQAHLRILKZTEFKKVKVKJGSGAFGTVYKGLMIPEGEKVKIPVAIKE--LREATSPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKEILDEAYVMAGVGSPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-profein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.1%; Score 1633.5; DB 1; Length 50.2%; Pred. No. 1.4e-80; ive 79; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E705E33A0BE01FCC CRC64;
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                         EMBL; M10066; AAA48763.1; ALT_INIT
                                                                                                                                                                                                                                                            PIR; A00643; TVCHLV.
PIR; B00643; TVFVLV.
HSSP; PI1362; IFCK.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation.
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Matches 356; Conservative
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165
257
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257
634 AA;
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21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase transforming protein erbB (BC 2.7.1.112).

634

PRT;

STANDARD;

Viruses, Retroid viruses, Retroviridae, Alpharetrovirus

Avian leukosis virus

ERBB ALV 1D ERBB ALV AC P00534. DT 21-JJL-198 DT 15-JJL-199 DT 15-JJL-199 DF Tyrosine-F GN V-ERBB. OC Avian leuk OC Viruses; F CN NCBI\_TAXIERR.

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-MNKTQ-----GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PL 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
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                                                                                                                                                                                                                             EPIDERMAL GROWTH FACTOR RECEPTOR
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                                                                                                   SMART; SM00261; FU; 4.

PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.

PROSITE; PS00109; PROTEIN KINASE TYR; PARTIAL.

PROSITE; PS50011; PROTEIN KINASE DOM; PARTIAL.

Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

Tyrosine-protein kinase; ATP-binding; Phosphorylation.

SIGNAL
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POTENTIAL.

CYTOPLASHIC (POTENTIAL).

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 EGFR L domain
                InterPro; IPR000719; Buk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00757; Furin-like; I.
Pfam; PF01030; Recep_L_domain; 2.
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>703
654
667
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214
230
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703 AA;
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Best Local Similarity
Matches 316; Conserv
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                                                                                                                        TFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLG 1056
                                                                                                                                                                                                                                                               1112 VPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSP 1169
                                                                                                                                                                                                                                                                                                                                  GKNGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNL 1214
                                                                        PPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHLPSPTDS 415
                                                                                                                                                                                                                450 -----SRTPLLSSLSALSNNSATNCID------RNGQGHPVREDSFVQRYSSDPT 493
                  VPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQ 355
                                                                                                                                                                                                                                                                                                                                                                VONOIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNOSPLAKTVFESS 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPT
                                                  PPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                    1215 YYWDQ------DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.7.1.112) (CER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANBOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                            -----NSPST-
                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC
                                                                                                                                                                                                                                                                                                GNFLEESIDDGFL-----PAPEYVNQ--LMPKKPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703 AA
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20386; AAA48760.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
                                                                                                                                                                                           1057
                   596
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EMBL; K01216; AAA42400.1; -.
PIR; A00644; TVVUH.
HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr_pkinase.
ProDons; PD00069; pkinase; 1.
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TELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLOVFETLEEITGYLYISAWPDS 418
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DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
                                                                                     TVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                              PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKF1G1
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MEDLINE-84223957; PubMed=6328658;
Debuire B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals new type of oncogene.";
Science 224:1456-1459(1984).
-: CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H;
MEDLINE=84026539; PubMed=6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima The erbB gene of avian erythroblastosis virus is a member of the gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBL_TaxIb=79685;
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MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-Yrosaine-protein kinase transforming protein erbB
V-ERBB.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between the Swiss Institute. There are or extrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQBRELVBPLTPSGE 117
----VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL------NTNQSPLAKTV 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706 MPNOAOMRILKETELRKVKVLGSGAFGQYIK----ANSKFIGITELVLRENTSPKANK 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP--- 58
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINEs97064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbs confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                             Viruses, Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                         (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%; Score 1520; DB 1; Length 5 52.7%; Pred. No. 1.4e-74; ive 68; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P11362; 1FGK.
InterPro; IPR001919; Buk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pro00m; PD0000001; Buk pkinase; I.
SWART; SW00219; TyrKc; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00109; PROTEIN KINASE TYR; I.
PROSITE; PS0010; PROTEIN KINASE DOM; I.
PROSITE; PS00011; PROTEIN KINASE DOM; I.
PROSITE; PS00011; PROTEIN KINASE DOM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB
                             1211 FDNLYYWDQDPPERGAPPSTFKGTPTAENPEY 1242
                                                                                                                                  540 AA
                                                                                                                                                                                                                                   Avian erythroblastosis virus (strain ts167)
                                                          --INLDNPDY
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                                                                                                                                  STANDARD;
                                                       573 FESSPYWIOSGNHO
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257
270
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DOMAIN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326;
                                                                                                                                  ERBB AVIEU
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VARIANT
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ERBB AVIEU
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118 APNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELREATSPKANK 177
                                                                                                                                                                                               298 IKWMALESILHRIYTHQSDVHSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP
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                                                        EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                       CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
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Search completed: July 22, 2003, 09:18:49 Job time : 16.5911 secs

Sequence:

Run on:

Database

Result Š.

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Q9ese0 rattus norv
Q9psh2 gallus gall
Q14255 homo sapien
Q923v5 rattus norv
P11776 xiphophorus
                                                                                                                                                                                                                                                                                                  QBSZW1 drosophila
Q99162 xiphophorus
Q99162 xiphophorus
Q9bd6 oryctolagus
Q9pvz4 xenopus lae
Q9njvs biomphalari
QBuw85 paralichthy
Q9use8 paralichthy
Q9use8 bombyx mori
QBuw84 paralichthy
Q73798 xenopus lae
Q9uw84 paralichthy
Q9ygh8 scophthalmu
Q9ygh8 scophthalmu
Q9ygh8 scophthalmu
Q9ygh4 rattus sp.
Q9umq4 drosophila
Q9tym0 mus musculu
Q9tyg4 drosophila
Q9tf35 homo sapien
Q96135 homo sapien
Q96135 homo sapien
Q9y1x8 ephydatia f
Q90836 gallus gall
Q23821 caenorhabdi
Q26566 schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dcg).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q991X8
Q90836
Q20836
Q26566
Q96560
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Q14256
Q12776
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Q9917V3
Q99164
Q9917V3
Q9917V3
Q9017V3
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Q9QVW4
Q9UMQ4
Q91YM0
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Q96L35
Q99MR2
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09uk79 homo sapien
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08ryv0 homo sapien
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                  GAGSDVFDGDLGMGAAKGLQSLPSQDPSPLQRYSEDPTVPLPPETDGKVAPLTCSPQPEY
                                                                                                                                                                                                EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
                                                                                                                                                                       VNQPDVRPQPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVVKDVFAFGGAVENP
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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InterPro; IPR000494; EGFR L domain.

InterPro; IPR00019; Euk pkinase.

R InterPro; IPR001245; TYL pkinase.

R InterPro; IPR001245; TYL pkinase.

R Pfam; PF001030; Recep_L domain; 2.

R Pfam; PF01030; Recep_L domain; 2.

R PRIMTS; PR00109; TYRKINASE.

R RSMART; SM00201; Euk pkinase; 1.

R RSMART; SM00219; TYKC, 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYP: 1.
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STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitred (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37394; AAF14008.1; -.
HSSP; P11362; 1FGK.
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STRANT=FISHER; TISSUE=LIVER;
Petch L.A.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
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Pred. No. 8.6e-221;
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Best Local Similarity
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                                                                                                1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                      Gaps
                                                   14;
  Length 1259;
                                                 75; Indels
       ..
    03
                                                 44; Mismatches
  89.9%; Score 6091;
89.5%; Pred. No. 0;
Query Match
Best Local Similarity 89.5
Matches 1128; Conservative
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| OY 1068 PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP   | RESULT 3 Q9EP98 ID Q9EP98 AC Q9EP98, DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence DT 01-WAR-2002 (TrEMBLrel. 21, Last annotatio DT 01-WAR-2004 (TrEMBLrel. 21, Last annotatio DE Epidermal growth factor receptor isoform 1 GN EGFR. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Ve OC Mammalia; Eutheria; Rodentia; Sciurognathi | •  | RA Reiter J.L., Threadgill D.W., Eley G.D., S Aschell C., Pearsall R.S., Green F.J., Yee RA Balasubzamaniam S., Crossley T.O., Magnuso RA Maihle N.J.; Crossley T.O., Magnuso RT "Comparative genomic sequence analysis and RT mouse alternative Egfr transcripts encodin RT isoforms."; Defense EMBL, Re75366; AAG28045.1; JOINED. DR EMBL, AR275366; AAG28045.1; JOINED. DR EMBL, AR275365; AAG28045.1; JOINED. DR EMBL, AR275365; AAG28045.1; JOINED. DR EMBL, AR275367; AAG28045.1; JOINED. DR EMBL, AR275367; AAG28045.1; JOINED. DR EMBL, AR275367; AAG28045.1; JOINED. DR HSSP, P11362; 1FGK. DR MGD, MGI:9524; EGK. DR MGD, MGI:95244; EGKR. DR InterPro: IPR0004345; Cyt.C. heme_bind. DR InterPro: IPR0004345; Cyt.C. heme_bind.   |   |
|---|---|--|--|---|
| Matches   629;   Conservative   165;   Mismatches   360;   Indels   126;   Gaps   31;   Gy   3   LAALCRWGLLALLPPGA-ASTQVCTGTDMKLEPASPETHLDMLRHLYQGCQVVQGNLE | QY 240 CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTXNTDTFESMPNFEGRYTFGASCVTAC 299   | Db 414 WTDLHAFENLEIIRGRTKQHGQFSLAVVGLNITSLGIASLKEISDGDVIISGNRNLCYAN 473  Qy 479 TVPWDQLFRNPHQALLHTANRPEDECVGEGLACHCARGHCWGPGPTQCVNCSQFLRGQ 538 | QY         658 UVGILLUVVLGGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK 716           BD         651 IVGGLLFIVV-VALGIGLFMRRQLVRKTLRRLLQERELVEPLTPSGAPNQAULRILK 709           QY         717 ETELRKVVLGSGAFQQYIKANSKFIGITELVLRENTSPKANKEILDEAYW           PD         710 ETERKXVKVLGSGAFGQYIKANSKFIGITELVLRENTSPKANKEILDEAYW           PD         769 AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS           QY         769 AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS           DD         768 ASVDNPHVCRLGICLTSTVQLTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMN           QY         829 YLEDVRLVHRDLAARNVLVKSPNHVKTTDFGLARLLDIDETEYHADGGKVPTKWMALESI           QY         829 YLEDRRLLARRNVLVKSPNHVKTTDFGLARLLDIDETEYHADGGKVPTKWMALESI           QY         828 YLEDRRLVHRDLAARNVLVKSPOHVKTTDFGLARLLCAREKRYHAGGGKVPTKWMALESI | 889 LRRRFTHOSDVWSYGVTVWELMTGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMI |

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DPSPLORYSEDPTVPLPSET--DGYVAPL 1125
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EDAFLORYSSDPTSVLTEDNIDDTFL--- 1086
                                                                    AGATLERAKTLSPGKNGVVKDVFAFGGAV 1185
| | : : | |
LHP-----APGRDLHYQN--PHSNAV 1132
                                                                                                                                               YWDQ-----DP-----PERGAPP 1228
                                                                                                                                                                       | | : | : | : | : | E.MIQKGSHQMSLDNPDYQQDFFPKEAKPN 1183
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e D., Lampland A.L.,
son T.R., James C.D.,
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hi; Muridae; Murinae; Mus.
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MIDSECRPRFRELVSEFSRMARDPQREVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLV 1012
                                              1014 DADBYLTPQQGFF----SRTPLLSS 1039
                                                                                                                                                       EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQ 1130
                                                                                                                                                                        | | | : : | | : : | | 1040 LSATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFL-----PV 1089
                                                                                                                                                                                                                                                                                                           LNTAQ------PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFKG 1189
 894 THOSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCW 953
                                                                                                                                                                                                                                     DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPS
                                                                                                                                                                                                                                                                              L-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----PERGAPPSTFKG
                                                                                                                                                                                                                   PEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., D Altschmied J., Schartl M.;
Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations.";
Oncogene 16:1681-1690(1998).
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InterPro; IPR0001345; CytC heme bind.
InterPro; IPR000139; Euk_Pinae.
InterPro; IPR0001374; Furin-like.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001295; Gram_pos_anchor.
InterPro; IPR001295; Tyr_pkinase.
InterPro; IPR001295; Tyr_pkinase.
IPEm; PF00757; Furin-like; 1.
Pfam; PF001030; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE.
ISWART; SW00219; TYRKINASE.
ISWART; SW00219; TYRCINASE.
ISWART; SW00139; TYRCINASE.
ISWART; SW00139; TYRCINASE.
ISWART; SW00139; TYRCINASE.
ISWART; PROSITE; PS00139; GRAM_POS_ANCHORING; UNKNOWN_1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                            -PTAENAEYLRVAPP 1203
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
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STRAIN=RIO PURIFICATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  422
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                                                                                                                                                                                                                                                                                                                                                      DINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVFONLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 DOLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKLFGTPNOKTKIMNNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDCVSCQNVSRGRECVE 537
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                                                                                                                                                                                                                                69 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                                                                                                                                                                                                                           129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGIL 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELR 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKE--LREATSPKANKEILDEAYVMASVDN 773
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                                                                                                                                                                   11 LILLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 68
                                                                                                                                                                                     74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDL
                                                                                                                                        Gaps
                                                                                                                                       122;
                                                                                                       Length 1210;
                                                                                                                                       Matches 620; Conservative 167; Mismatches 366; Indels
            PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
                                                                                                       44.3%; Score 2999; DB 11; 48.6%; Pred. No. 1.4e-218;
 PS00190; CYTOCHROME C; UNKNOWN 1.
                                                                                                                       Similarity
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------EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNT 1105
                                                                                                                                                                                                                                                                                                               1170 GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1229
                                                                                                                                                                                                                                                                                                                                                1106 NONSL---PLVSSGSMDDPDY---QAG-----YQAAF-----LPQTGALTG 1140
                                                                                              EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1063
                                                                                                                                                                                                       1123 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP
                          DVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLL
                                                                                                                                                                   .064 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                  ------RYKRIN-RQGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 1137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99263203; PubMed=10328884; Dixon M., Lumsden A.; "Distribution of newregulin-1 (nrgl) and erbB4 transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4D616436F87DC84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%; Score 2577.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM0019; Tyrk; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryonic chick hincbrain.";
Mol. Cell. Neurosci. 13:237-258(1999)
EMBL; AF121963; AAD31764.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IRR000494; EGFR L domain.
InterPro; IRR000119; Euk Pkinase.
InterPro; IRR0012194; Furin-11ke.
InterPro; IRR001368; TNFR C6.
InterPro; IRR001245; TVF pkinase.
InterPro; IRR004019; YLP motif.
Pfam; PF00757; Furin-11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor tyrosine kinase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Buk pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain; 1.
Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinase, Tyrosine-protein kinase.
NON TER 1 1 SEQUENCE 1137 AA, 127927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            1141 NGMFLPAAENLEYLGL 1156
                                                                                                                   1230 TFKGTPTAENPEYLGL 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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Q9W6F6;
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                                                                                                                                                                                                                                                                             TSNPTMNLIPHAFERQCQKCDPGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGPKPID 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 175
                                                                                                                                                                                                                                                                                                                                                                                                  NNOLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRIVCAGGC-ARCKGPLPTD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGM----QYI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 YISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIH 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIMWWPENMTSLSVFQNLEIIRGRTTFSRGFSFVVVQVSHLQWLGLSSLKEVSAGNVILK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 YKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRAS 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLLQETELVEPLTPSGAMPNQ 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQMRILKETELRKVKVLGSGAFGQYIK-----ANSKFIGITELVLRENTSPKANKEILD 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWM 883
                                                                                                                                                                                                          CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 KANSKFIGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCIHVDRGGRCVASCNILLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCSKCAH
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                                                                                                                                                                                    1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
                                                                                                                                                  Gaps
                                                                                                           Query Match 38.5%; Score 2611; DB 13; Length 1165; Best Local Similarity 44.5%; Pred. No. 3.8e-189; Matches 568; Conservative 162; Mismatches 392; Indels 154;
PROSITE, PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 2.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1165 AA; 129614 MW; 7F7EE33B08771A74E CRC64;
                                                                                                                                                                                                                                                         26
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1010 GDLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLENAEYL----- 1054
                                                                                  KNNLPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKPCARVCYGLGMQYIKANSKFIGIT 360
                                             --- AENPEYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WRLILMCVASRLRAASSQTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
                                                                                                                                                                                                                                                                                                  Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Taleostei; Buteleostei; Neoteleostei.
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198;
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EMBL, AF065116; AAC34391.1; -.

EMBL, AF065116; AAC34391.1; -.

EMBL, AF065116; AAC34391.1; -.

EMBL, AF065116; AAC34391.1; -.

EMBL, AF06716; EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN_EMF_DEN
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ErbB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.3%; Score 2191; DB 13; Best Local Similarity 39.2%; Pred. No. 3.6e-157; Matches 504; Conservative 158; Mismatches 427;
                                             OPHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT
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                                                                                                                                                                                    1328
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99177347, Pubmed=10077531;
Gellner K., Brenner S.,
"Analysis of 148 kb of genomic DNA
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31033;
                                             1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRHRSSSTRSGGGDLTLGLEPSEEEAPRS--PLAP-SEGAGSDVFDGDLGMGAAKGLQSL 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPRE 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----AFGGAVENPEYLTPQGGAAP 1199
                        27;
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                                                                                                                                                                                                                                                359 GCWGPGPDQCLSCKRPIRGRTCIESCNLYDGEPREFANGSVCMECDPQCEKMEDDMITCY 418
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                                                                                                                                          AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF 279
                                                                                                                                                                 ESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA 339
                                                                                                                                                                                                                                                                                                      RVCYGLGMQYIKANSKFIGITELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQ 398
                                                                                                                                                                                                                                                                                                                                                                                   VFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSL 458
                                                                                                                                                                                                                                                                                                                                                                                                         RELGSGLALIHHNTHLCFVHTVPWDQLPRNPHQALLHTANRPEDECVGEGLACHQLCARG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 GPGPDHCTKCFHFKDGPNCVEKCPDGLQGANSF--IFKYADEDRECHPCTQGCRGP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGQYIK-----ANS 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 KFIGITELVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGC 799
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832 YLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVP-QAFNIPPPIYTSRTRID
                                                              LCYQDT1LWKD1FHKNNQLALTL1DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
                        Gaps
                          85;
    45.4%; Pred. No. 1.3e-186; ive 174; Mismatches 363; Indels
                      518; Conservative 174;
Best Local Similarity
Matches 518; Conserv
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141 QLRSLTEILKGGVLIQRNPQLCYQDTILWKDI-FHKNNOLALTLIDTNRSRACHPCSPMC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELEFAGCKKIFGSLAFL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAHNQVRQVPI,QRLRIVRGTQLF - - - - EDNYALAVLDNGDPLNNTTPVTGASPGGLREL
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                       Anopheles gambiae (African malaria mosquito).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                            "Cloning, expression and localisation of the Anopheles gamb epidermal growth factor receptor."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ301655; CAC35008.1; -. HSSP; P11362; IFGK. InterPro; IPR000345; CytC, heme, bind. InterPro; IPR000494; EGREL_J domain. InterPro; IPR000719; Buk, pkinase. InterPro; IPR000719; Furin-like. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. Pfam; PF00059; pkinase; 1. Pfam; PF01030; Recept_L domain; 2. Pfam; PF01030; Recept_L domain; 2. ProDom; PR000001; Eik_pkinase; 1.
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1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
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SMART; SM00261; FU; 7.
SMART; SM00220; S_TC; 1.
SMART; SM00219; TYZC; 1.
PROSITE; PS00190; C'TOCCIROME C; UNKNOWN 4.
PROSITE; PS00101; PROTEIN KINASE_ATP, 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.
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Best Local Similarity
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=7165;
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                                                                                                                      103 NDLSVPSSLTTIQGRSLFKRFSLMVMRIPTLTSLGLRSLREISDGSVVISONAHLCYHHT 462
                                                                                                                                                                                                                  TCVAGCHFINSGI PREFAGLINGVCVACHPECKPQTGKASCTGPGADECMACTKFRDGPYCM 582
                                                                                                                                                                                                                                                                                                                                                                                             SCPAGVN-DGEKGLIFKFPNREGHCEPCHQNCTQGCSGPGLNDC---LEAARLTISSGQ 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLSMGSLDHPYIVRLLGICPGTCLQLVTQLSSHGSLLEHIRQHKTSLDPQRLLNWCVQIA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ 538
                                                                                                                                                                                                                                                                                                                                                                        ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVGILLVVVLGVVF-----GILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQA 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
                              ECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GLGDRFATPSLQPSPSWSTSPSQINSYMVMTQLRYD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1065 PRSPLAPSEGAGSDVFDGDLGMG---AAKGLQSLPTHDPSPLQ-----RYSEDPT
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                                                                                              PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSELH9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1112 VPLPSETDGYVAPLTCSPQP-EYVNQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1215 YYWDQDPPERGAPPSTFKGTPTAENPE 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                        562 NGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLMKDESCPDGYYSDYVL 621
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                     SDHEVMVQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLDSCK--- 506
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                                                                                                                                                                                                                           ------RASPLTSIVSAVVGILLVVVLGVVFGI---LIKRRQQKIRKYTM 687
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                                                                                        --SGVKPDLSYMPIWKFPD-----
                                           GLPREY-VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP----
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Q9UK79 Q9UK79; RESULT 8 % Q9UK79 ID Q9UK79 AC Q9UK79;

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ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR17761; AAD56009.2; -
InterPro; IPR00494; EGRR, L. domain.
InterPro; IPR002174; Furin-like.
Pfan; PF00757; Furin-like; 1.
Pfan; PF01030; Recep L. domain; 1.
SMART; SM00261; FU; I.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-9941551; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                      Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kBa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
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Matches 341; Conservative
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  (TrEMBLrel.
                      01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFG 300
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REQUENCE FROM N.A.

RECURSITION B., RAYDOSCHECK C., Jansson L., Doederlein G., Lhotak V.,

A Venistron B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,

RA Johnsson A., Beug H.;

Retroviral capture of c-erbB proto-oncogene sequences: rapid

RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid

RT different transforming capacities.";

Chocogene 9:1307-1320(1994).

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; AAC60725.1; -.

REL. 569372; Retro M.

RINEEPRO; IPRO0124; Retro M.

RINEEPRO; IPRO0124; TY- DRINASE.

REAM; PRO0069; pkinase; 1.

REAM; PRO0009; pkinase; 1.

REAM; PRO0019; PROTEIN KINASE ATP; 1.

REAM; PROSITE; PS00107; PROTEIN KINASE TYP; 1.

RESORTE; PS00109; PROTEIN KINASE TYP; 1.

REPOSITE; PS00109; PROTEIN KINASE TYP; 1.

REPOSITE; PS00109; PROTEIN KINASE TYP; 1.

REPOSITE; PS00109; PROTEIN KINASE TYP; 1.

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REPOSITE; PS00109; PROTEIN KINASE TYP; 1.

REPOSITE; PS00109; PROTEIN KINASE TYP; 1.

REPOSITE; PS00109; PROTEIN KINASE TYP; 1.
                                                                               942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628
                                                                                                                        1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                983 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
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       53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 WVWTCQCEPEGOVRRSPDVSSGSREGLTSAGIKRWEGPPTTSRGTCHARN 410
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           22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
       5; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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       Matches 330; Conservative
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Q86712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LEDDDWGELVDAEEYLVPQQGFFSPDPALGTGSTAHRRHRSSSARSGGGELTLGLEPSEE 180
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                                                                                                                                                                                                                                                                                                                                 943 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                                                                                           883 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
Wan D.F., Gu J.R.,
"Novel human cDNA clones with function of inhibiting cancer cell
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                                                                                                                                           Query Match 25.7%; Score 1739; DB 11; Length 367; Best Local Similarity 88.0%; Pred. No. 1.1e-123; Matches 323; Conservative 11; Mismatches 33; Indels 0
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EMBL; AF318349; AAL55856.1; -
InterPro; IPR002048; EF-hand.
InterPro; IPR001019; EV-pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; Yup motif.
Pfan; PF00699; pkinase; I.
ProDom; PD000001; Euk_pkinase; I.
SWART; SM00219; TyrKc; I.
PROSITE; PS00011; PRŌTEIN_KINASE_DŌM; I.
                                         ll protein.
367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
EMBL; BC027080; AAH27080.1; -. Hypothetical protein. SEQUENCE 367 AA; 40163 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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QBWYVO; QBWYVO

RESULT 10

18;

Query Match

18;

Gaps

637

57

969 113 808

868 291

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988 LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTR 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDL 928
                                                                                                                                                                                                                                                                                                                                                                                        58 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
                                                                                                                                                                                                                                                                                                           578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                                                                                                                                                 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1103 LQRYSEDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT
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the
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Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=11861;
                                                                                                                                                                                                                                    112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman I strain acids from the retroviral gene gag greatly enhance transforming potential of the oncogene v-erb-B.";
                                                                                                                                                                                            Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1161 LERAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1191
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Last annotation update)
                                                                                                                                                                                       23.6%; Score 1602; DB 15;
Local Similarity 53.1%; Pred. No. 5.3e-113;
les 343; Conservative 73; Mismatches 118;
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R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

W Tyrosine-protein kinase.

NON TER

SEQUENCE FATTER
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                           314 IPVAIKE--LREATSPKANKEILDEAYVMASVDNPRVCRLLGICLTSTVQLITQLMPYGC 371
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                                                                                                                           LLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDG 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM 687
                                                                                                                                                                                         RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGQ-----YIKANSKF- 741
                                                            PEETATPKTGP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCOLCHP 197
                                                                                                                                                                                                                                                                          --IGITELVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGC
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"Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes different transforming capacities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11950;
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InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PR00109; TYRKINASE.
ProDom; PR000001; Euk pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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MEDLINE=94203659; PubMed=8152791;
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HSSP; P11362; 1FGK.
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22.7%; Score 1535; DB 15; 52.5%; Pred. No. 6.2e-108; ive 69; Mismatches 131;
                                                           -LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1191
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InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Buk pkinase; 1.
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Best Local Similarity 52.5%
Matches 330; Conservative
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Q85468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTL 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762 ASEISSVLEKGERLPQPPICTIDVYMIMVKCWMSGADSRPKFRELIAEFSKWARDPPRYL 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   867 -NSPST------SRTPLLSSLSATSN-----NSATKCIDRNGGH-- 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
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             SIMILARITY).
HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                    22.8%; Score 1543.5; DB 15; Length 962; 49.6%; Pred. No. 3.3e-108; Live 72; Mismatches 152; Indels 125;
                                                                                                                                                                                                                                                                                                        Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                               962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
                                                                                                                                                                                                                                  SMART; SM00199; ZAF C4; 1.
PROSITE; PS00031; NUCLERA RECEPTOR; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DW; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; DNA-binding; Nuclear protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                   VEECRVLQGLPRE-YVNAR-HCLP-------
                               EMBL; X52209; CAA36459.1; EMBL; X52211; CAA36459.1; EMBL; X52211; CAA36459.1; JOINED. HSSP; P10829; 2MLL. InterPro; IPR000719; Buk pkinase. InterPro; IPR001723; Stdhrum:receptor. InterPro; IPR0010723; Stdhrum:receptor. InterPro; IPR001048; Tyr pkinase. InterPro; IPR001628; Zf C4steroid. Pfam; PP00104; hormone_rec; 1. Pfam; PP00105; zf-C4; 1.
Oncogene 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY S
-!- SIMILARITY: BELONGS TO THE NUCLEAR
                                                                                                                                                            PRINTS; PR00398; STRDHPRMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD0000001; Euk pkinase; 1.
ProDom; PD0000001; Euk pkinase; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00219; TYFKC; 1.
SMART; SM00319; ZNFC C4; 1.
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                                                ----PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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MEDLINE=88217326; PubMed=2897102;
SCOLLINE=88217326; PubMed=2897102;
SCOLLING=88217326; PubMed=2897102;
Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation."; Oncogene Res. 1:265-278(1987).
EMBL; X06943; CAA30024.1; -.
HSSP; Pl1362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBL_TaxID=11861;
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PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 545 AA; 60899 MW; 140DCESCCA0F8AF4 CRC64;
                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (TS34) v-erbB gene.
Avian erythroblastosis virus.
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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Selya T., Shibata Y., Storch K.-F., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M., Wanshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
990 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1049
                                                            1050 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1104
                                                                                                                                            --NSPST--- 454
                                                                               STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Retter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative genomic sequence analysis and isolation of human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
              414 LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF---
                                                                                                                                                                                    1164 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 HFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 KKLFGTPNÓKTKIMNNRAEKDĆKAVNHVĆNPĽĆSSEGČWGPEPRDČÝSČQNVSRGREČVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECRVLOGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 -FAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLOVFETLEEITGYLYISAWPDSLPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 655;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.2%; Score 1506.5; DB 11; Lengt
Best Local Similarity 44.5%; Pred. No. 1.2e-105;
Matches 285; Conservative 97; Mismatches 233; Indels
                                                                                                                                                                                                                                                                                                                                                       655 AA; 72906 MW; 6B34063B1BC928CB CRC64;
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EMBL; AF27536; AAG28047.1; --
EMBL; AF275364; AAG28047.1; JOINED:
EMBL; AK275365; AAG28047.1; JOINED:
EMBL; AK004444; BAB23468.1; --
EMBL; AK004883; BAB23481.1; --
EMBL; AK004911; BAB23662.1; --
                                                                                                                                                                                                                 IncerPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
SMART; SM00261; FU; 3.
                       Nature 409:685-690(2001
                                                              EMBL; AF275366; AAG2804
EMBL; AF275364; AAG2804
EMBL; AF275365; AAG2804
EMBL; AK004944; BAB2368
EMBL; AK004983; BAB2364
EMBL; AK004911; BAB2364
MGD; MGI:95294; EGIT.
                                                                                                                                                                                                                                                                                                              SMART; SM00261; FU;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| Run on: July 22, 2003, 08:41:54; Search time 36.7573 Seconds  Run on: July 22, 2003, 08:41:54; Search time 36.7573 Seconds  (without alignments)  4527.811 Million cell updates/(Title: SEQ4-710-730-12  Perfect score: 6775  Sequence: 1 MELAALCRWGLLLALLPPGATFKGTPTAENPEYLGLDVPV 1249 |
|---|
| Scoring rable. BLOSIM62   |

scoring table: bLOSUN62 Gapop 10.0 , Gapext 0.5 Searched: 908470 segs, 133250620 residues Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| ID Description                     |      |      | AAB60167 HER2 transgene p |      |      |      | AAB21198 Human HER-2/neu pr |      |      |   |
|------------------------------------|------|------|---------------------------|------|------|------|-----------------------------|------|------|---|
| DB                                 | 21   | 22   | 22                        | 23   | 17   | 20   | 21                          | 21   | 22   | Ċ                                       |
| Length                             | 1255 | 1255 | 1255                      | 1255 | 1255 | 1255 | 1255                        | 1255 | 1255 | ייייייייייייייייייייייייייייייייייייייי |
| %<br>Query<br>re Match Length DB I | 97.5 | 97.5 | 97.5                      | 97.5 | 97.4 | 97.4 | 97.4                        | 97.4 | 97.4 | 7 70                                    |
| Score                              | 6608 | 6608 | 8099                      | 6608 | 6602 | 6602 | 6602                        | 6602 | 6602 | 6603                                    |
| Result<br>No.                      | 1    | 7    | ٣                         | 4    | S    | 9    | 7                           | œ    | σ    | -                                       |

| Her-2 prot<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>nce of c-er<br>Dreagt can<br>BER-2/neu pr<br>er-2/neu on<br>Her-2/neu<br>Acid seque<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Cellular HE<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu<br>Her-2/neu   | Human Her-1 protei<br>Human epidernal gr<br>Amino acid sequenc<br>Human epidernal gr<br>Human protein for<br>Human protein for |
|---|--|
| AAE2047<br>AAE2047<br>AAB5114<br>AAU77114<br>AAB2139<br>AAB2139<br>AAB2119<br>AAB2120<br>AAB2120<br>AAB2120<br>AAB2120<br>AAB2120<br>AAM5115<br>AAM5115<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116<br>AAM5116   | 3 AAE23019<br>AAM50768<br>2 AAM66420<br>3 ABP51768<br>3 AAE20483<br>AAE20481   |
| 1255 23<br>11255 23<br>11255 23<br>11255 23<br>11255 23<br>11256 22<br>11256  | 1210<br>1210<br>1210<br>1210<br>583<br>583<br>2  |
| 00000000000000000000000000000000000000  | 444444<br>7.7.4444<br>7.1.44.84<br>7.1.1.7.0   |
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|   | 4 4 4 4 4<br>0 4 5 6 6 6 6   |

## ALIGNMENTS

|   |               |                           | phocyte immunity;<br>ancer;<br>e.  |               |               | itope insertion"  | itope insertion"  | itope insertion"  | epitope insertion"  |
|---|---------------|---------------------------|--|---------------|---------------|---|---|---|---|
| T 1<br>620<br>AAY92620 standard; Protein; 1255 AA.<br>AAY92620; | (first entry) | in 2 (Her2).              | Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope. |               | ~ "           | /noce= "mature polypeptide"<br>525<br>/label= insertion region<br>/note= "suitable for foreion epitone insertion" | 5973 /label= insertion region /note= "suitable for foreign epitope insertion" | 103117<br>//label= insertion region<br>/note= "suitable for foreign epicoe insertion" | 149163<br>/label= insertion region<br>/note= "suitable For foreign ep<br>174323 |
| LT 1<br>2620<br>AAY92620 stand<br>AAY92620;                     | 10-AUG-2000   | Human heregulin 2 (Her2). | Heregulin 2; F<br>self-protein;<br>cell-associate  | Homo sapiens. | Key<br>Domain | Region  | Region  | Region  | Region<br>Domain  |
| RESULT 1 AAY92620 ID AAY XX AC AAY                              | <b>4</b> E 3  | S E S                     | \$ \$ \$ \$  | ×8 ×          |               | FT  | FFF   | 111   | FT<br>FT<br>FT  |

seq4-710-730-12.rag

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cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APC8) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDGCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEBCRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILLVVVVLGVVFGILIKRRQOKIRKYTMRRLLOETELVEPLTPSGAMPNOAOMRILKETEL
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWDOLFRNPHOALLHTANR PEDECVGEGLACHOLCARGHCWGPGPTOCVNCSOFLRGOEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKVKVLGSGAFGQY1KA-----NSKF1G1TELVLRENTSPKANKE1LDEAYVMAGVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with
                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                               Length 1255;
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Pred. No. 0;
5; Mismatches
                                                                                                                                                                                                                                                                                                         97.5%;
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Best Local Similarity 97.4
Matches 1223, Conservative
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| Jabel= insertion region
| Jace= "suitable For foreign epitope insertion"
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/label= insertion region
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|label= insertion region
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/label= insertion region
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|Jabel= insertion region
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label= Tyrosine_kinase_domain
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| Tabel = Ligand_binding_domain
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|Jabel= insertion region
|note= "sultable For foreign
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label = Cysteine_rich_domain
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Birk P, Karlsson G;
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98US-0105011.
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                                                          The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polymucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of some transcripts that are expressed in antigen presenting cells (APCS), to confirm transduction of polymucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds
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llarity 97.4%; Pred. No. 0;
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                                 PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
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               PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
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                    The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HBF and p185neu). The method is particularly useful in the treatment of breast, ovarian, stonach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers
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16-MAR-2000; 2000US-0189844.
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is characterised by the overexpression of an epidermal growth factor receptor (BTbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating environal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                    Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host calls for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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                           839
                                                                                                                                                                                 THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW 959
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RLVHRDLAARNUVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRF
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676..1255
/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
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the HER-2/neu oncogene is
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          of this protein is used in a method for eliciting or enhancing an imm response to HBR-2/neu protein. The polypeptide can stimulate T cells B cells to produce an immune response to the HBR-2/neu protein. The method can be used for immunisation against a malignancy in which the HBR-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                                                                                                 Gaps
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                                                                                                                                                           GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY 1133
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                                                                                                                                                                                                               VNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1193
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                                                                                                                       AEEYLVPQQGFFCPDPAPGAGGWYHRRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE
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THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW
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                                                   MIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVD
                                                                                                        AEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; cancer; prostate cancer; ovarian cancer; lung cancer;
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   Score 6602; DE Pred. No. 0; 6; Mismatches
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97.28;
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                                                               ABEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE
                                             AEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
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the protein are useful for
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                                                                                VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1193
                                                                                                The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2).
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                                                                                                                                          QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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Best Local Similarity 97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I), bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino caids that have look identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (II) comprising (II) and a pharmaccutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for inducing cellular immune response to a tumour-associated antigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient of consider that manuogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour sasociated molecules addressing the problem of tumour cumour variability and reducing the likelihood of tumour escape ducing the present annour variability and reducing the likelihood of tumour escape ducing the present invention.
 1140 VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1199
                                                                                                                                                                                                                                                                       Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated prepared {\tt HER2/neu} epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer -
                                                 QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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                                                 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                        GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HiA)-B4 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, preventions of cancer. The compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a length gene from a suitable library, and to direct expression of a length gene from a suitable library, and to direct expression of a length gene from a suitable library.
1140 VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVPAFGGAVENPEYLTP 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The present sequence is human Her-2/neu protein.
                                                                                                                                                                                                                              Human, Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                                          epitope"
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                                        QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                     Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted
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Mcneill PD, Vedvick TS;
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                                                                         1140 VNOPDVRPOPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTP 1199
1020 AEEYLVPOOGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSE 1079
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                                                                                                       QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor intracellular domain that also shows homology to EGFR). Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral-vectors, and vaccines
                  GAGSDVPDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSFTDGYVAPLTGSPQPEY
                                 1080 GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY
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                                                                                                                                                                                                                                                                Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185; tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                            Human Her-2/neu oncogene-encoded p185 glycoprotein.
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/note= "phosphorylation domain"
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/note= "extracellular domain"
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SMITHKLINE BEECHAM BIOLOGICALS
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preferred fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltapD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid cenceding the fusion protein, and delivering the transfected cells conceding the fusion protein, and delivering the development of a cancer, especially breast, ovarian, colon, lung or protein of a cancer in a patient. I cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
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Best Local Similarity 97.2
Matches 1221; Conservative
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360 420 420 540 540 009 99 999 720 720

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seq4-710-730-12.rag

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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Z/neu or a polyncleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hoddgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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                                                                                                            THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Her-2/neu; cytostatic; haematological malignancy; CML;
acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLI
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS,
Hodgkin's lymphoma; T cell therapy.
                                                                                                                                                                                                                                                                                                                                                                                                            QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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28-SEP-2000; 2000US-0675904.
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AEEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEBAPRSPLAPSE 1079
                                                  ELTYLPTNASLSFLØDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                    VEECRVLOGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                            MELAALCRWGLLIALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQVCQVVQGNL
                                                                                                                                                       AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                        YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCBKCSKPCARVCYGLGMQYIKANSKFIGIT
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                                                                     GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY
                                                                                                                                                                         VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTP
THQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYMIMVKCW
                                                           MIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVD
                                                                                            AEEYLVPQQGFFCPDPAPGAGGWVHHRHSSSTRSGGGDLTLGLEPSEEBAPRSPLAPSE
                                                                                                                                                                VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTP
                         THQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPPICT1DVYMIMVKCW
                                                                                                                              GAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY
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antigen - for imaging or treating breast or
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No. 0;
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Best Local Similarity
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        1074 GAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPOPEY 1133

        Db
        1080 GAGSDVFDGDLGMGAAKGLOSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPOPEY 1139

        Qy
        1134 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVPAFGGAVENPEYLTP 1193

        Db
        1140 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVPAFGGAVENPEYLTP 1199

        Qy
        1194 VGGAAPQPHPPPAFSPAFDNLYYWDQDPPRRCAPPSTFKGTPTAENPEYLGLDVPV 1249

        Db
        1200 QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

        Search completed: July 22, 2003, 09:16:55

        Job time: 42.7573 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec

Title: SEQ4-5-25-14
Perfect score: 6812 . Sequence: 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEXLGLDVPV 1255

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result |       | *<br>Ouerv |        |    | SUMMARIES |                    |
|--------|-------|------------|--------|----|-----------|--------------------|
|        | Score | Match      | Length | 80 | DI        | Description        |
|        | 6694  | 98.3       | 12     | н  | A24571    | protein-tyrosine k |
| S      | 879.5 | 86.3       | 7      | ~  | 148161    | p-185 precursor -  |
|        | 5876  | 86.3       |        | н  | TVRTNU    | protein-tyrosine k |
|        | 3132  | 46.0       | _      | -  | GOHUE     | epidermal growth f |
|        | 3111  | 45.7       |        | ~  | A53183    |                    |
| m      | 086.5 | 45.3       |        | Н  | TVCHLV    |                    |
| N      | 968.5 | 43.6       |        | 7  | A47253    | epidermal growth f |
|        | 2689  | 39.2       |        | Н  | S06142    | protein-tyrosine k |
|        | 2408  | 35.3       |        | ~  | A36223    | kinase-related tra |
| N      | 327.5 | 34.2       |        | ~  | JC4387    | epidermal growth f |
| ٦      | 766.5 | S          | 969    | Н  | TVFVLV    | protein-tyrosine k |
|        | 1703  | S          |        | -  | TVYUH     | protein-tyrosine k |
| Ä      | 652.5 | 4          |        | Н  | GQFFE     |                    |
|        | 1647  | 24.2       |        | ~  | S35745    |                    |
|        | 1640  | 24.1       |        | ~  | S00727    | kinase-related tra |
|        | 1623  | 23.8       |        | 7  | B44776    | protein-tyrosine k |
|        | 1621  | 23.8       |        | Н  | TVFVEB    |                    |
|        | 1505  | 22.1       |        | ~  | A36325    | epidermal growth f |
|        | 1297  | 19.6       |        |    | E88257    | et-23 [i           |
|        | 1297  | 19.0       | 1374   |    | S70712    | protein-tyrosine k |
|        | 1189  | 17.5       |        |    | S70713    | protein-tyrosine k |
|        | 1175  | 17.2       |        |    | A45558    | growth             |
|        | 1118  | 16.4       |        |    | A42032    | growth             |
|        | 953.5 | 14.0       |        |    | A27131    |                    |
|        | 806.5 | 11.8       |        |    | S13807    | protein-tyrosine k |
|        | 754.5 | 11.1       |        |    | S13808    | protein-tyrosine k |
|        | 724   | 0          |        | ~  | T43220    | insulin-like growt |
|        | 0     | 10.3       | 7      | H  | INHUR     | insulin receptor p |
|        | 699.5 | 10.3       | 1607   | ~  | T43212    | insulin-like growt |

| insulin receptor p | insulin receptor p | protein-tyrosine k | insulin receptor-r | insulin receptor-r | insulin-like growt | insulin-like growt | insulin receptor - | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | tyrosine kinase Mp | mouse developmenta | protein-tyrosine k | protein-tyrosine k |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A34157             | A36080             | T18534             | . A36502           | B36502             | IGHUR1             | A33837             | A56081             | T30346             | 857245             | A54092             | 150612             | S49004             | I48652             | 805582             | 833596             |
|                    |                    |                    | •                  |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
| ~                  | 7                  | 7                  | 7                  | 7                  | Н                  | 0                  | Н                  | ~                  | N                  | 7                  | 7                  | ~                  | 0                  | Н                  | 7                  |
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| •                  | _                  |                    |                    |                    | •                  |                    | •                  |                    | •                  |                    |                    |                    |                    | 8.6 1114 1         | -                  |
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## ALIGNMENTS

| · · · · · · · · · · · · · · · · · · · | RESULT 1  A24571  A24771  A247 |
|---------------------------------------|--|
|                                       | A, Residues: 812-999 kRs. A, Residues: 812-999 kRs. VID: 9459807, PIDN: AAA35809.1; PID: 9459808 A, Cross-references: GB: L29995, NID: 9459807, PIDN: AAA35809.1; PID: 9459808 R; Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell. Biol. 7, 2597-2601, 1987 A; Title: Human HBR2 (neu) pronoter: evidence for multiple mechanisms for transcriptiona A; Reference number: I37622; MUID: 87286898; PMID: 3039351 A; Accession: I57622 A; Statues: translated from GB/EMBL/DDBJ A; Residues: l-191 cTAL>  |

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p-185 precursor - golden hamster
C.Species: Mesocricetus auratus (golden hamster)
C.Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C.Accession: 148161
R.Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa Gene 140, 251-255, 1994
A.Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A.Reference number: 148161
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-1254 <RES
A.Coss-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
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                                                           ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG 776
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                                                                                                                                                                                                                                                                                                                                                                                 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV 956
VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIIS 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGD
                                        AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
                                                                                                                                                                                                  VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL
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                                                                                                                    ETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEI LDEAYVMAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.3%; Score 5879.5; DB 2;
86.2%; Pred. No. 8.9e-233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
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Matches 1085, Conservative
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C,Superfamily:
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Fig. 21/Domain: signal sequence #status predicted <8IG>
Fig. 21.255/Product: protein-tyrosine kinase erb82 #status predicted <RXT>
Fig. 25.455/Domain: extracellular domain repeat <EEL>
Fig. 20.45/Domain: EGF receptor extracellular domain repeat <EEL>
Fig. 25.50/Domain: EGF receptor extracellular domain repeat <EEL>
Fig. 25.50/Domain: intracellular #status predicted <IVMN>
Fig. 45.45/Domain: intracellular #status predicted <IVMN>
Fig. 45.45/Domain: protein kinase homology <RIN>
Fig. 12.41/Region: protein kinase ATP-binding motif
Fig. 13.4/Region: protein kinase ATP-binding motif
Fig. 686/Binding site: carbohydrate (Asn) (covalent) #status predicted
Fig. 686/Binding site: Lys #status predicted
Fig. 13.3/Active site: Lys #status predicted
Fig. 13.3/Local (Covalent) (by autophosphorylation)
                                                                                                                                                               C;Function:

Lybescription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C;Superfamily: epidermal growth factor receptor; protein kinase homology

C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
                        30
                        about
    PIDN:AAAS8637.1; PID:g553332
of this erbB-related gene occurs in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLISIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 QGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV
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98.3%; Pred. No. 5.4e-266;
iive 5; Mismatches 9;
                                              A,Gene: GDB:ERBB2; NGL; NEU; HER-2
A,Cross-references: GDB:120613; OMIM:164870
A,Map position: 17q21.1-17q21.1
A,Introns: 25/1; 75/3; 147/1; 883/3
K,Note: the list of introns is incomplete
C,Function:
A;Cross-references: GB:M16792; NID:g183983;
C;Comment: Amplification and overexpression
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.3
Best Local Similarity 98.3
Matches 1237; Conservative
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| The Modern Control Con | ·<br>66666   | QGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDN<br>   |   |
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| 297 TACPMYSTED TO SCHUTCHINGENTARD CROCKCSKO PARVCYGLOBERLAR WAN 356  297 THO PHYLLIP CASCILLY CHANGENTAR COTTON CROCK CASCILLING THE TOTAL TSAN DEPOCACILLY SAMP 416  357 TSAN TO SEA CHANGE THE SENGE AS SCHUTCH CASCILLING THE TOTAL TSAN PARCE AS A TOTAL CASCILLING THE TOTAL TSAN PARCE AS A TOTAL CASCILLING TO SCHUTCH CASCILLING THE TOTAL TSAN PARCE AS A TOTAL CASCILLING TO SCHUTCH CASCILLING T | 2 8 2 8      | NQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCC 23.  | RESULT 3 TVENTU TVENTU TVENTU PROTECTIVE Kinase (EC 2.7.1.112) neu precursor - rat C'Species: Rattus norvegicus (Norway rat) C'Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999 C'Accession: A24562; A61204 R'Bargmann, C.1.; Hung, M.C.; Weinberg, R.A.   |
| 357 TSANIORPAGCKKIPGSLAPLPRSPDODAASYTAPLOPDOLOVPETLEDITCKLYISAWP 416 357 TSANIORPAGCKKIPGSLAPLPSSPOODAASYTAPLOPDOLOVPETLEDITCKLYISAWP 416 417 DSLPDLSVPQNLQVIRGRILHNGAYSLTLQCLGISMLGLRSLRSLGSGLALHHNTHLCF 476 417 UNIVENDOLPRNPHQALLHTANRPEDECVORGLACHGLGRCHCGCPTQCVNCSQPLR 536 417 VHTVPWOQLPRNPHQALLHTANRPEDECVORGLACHGLGRCHCGCPTQCVNCSQPLR 536 417 VHTVPWOQLPRNPHQALLHTANRPEDECVORGLACHGLGRCHCGCPTQCVNCSQPLR 536 417 VHTVPWOQLPRNPHQALLHTANRPEDECVORGLACHGLGRCHCGCPTQCVNCSQPLR 536 418 CHILLI   | 상<br>음<br>상  | 97 TACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAV 35  | Nature 319, 226-230, 1986 A Fitle: The neu oncogene encodes an epidermal growth factor receptor-related protein. A Reference number: A24562; WUID:86118662; PMID:3945311 A Accession: A24562.   |
| 417 DSLPDLSVPQNLQVIRGRILHNGAVSLTLQGLGISMLGIRSLESGIALIHHNTHLCF 476 417 DSLPDLSVPQNLQVIRGRILHNGAVSLTLQGLGISMLGIRSLESGIAVIHHNTHLCF 476 417 DSLHDLSVPQNLRVIRGAVSLHGAVSLGLGGROPARGLGRGWDEPTQCVNCGPIR 536 417 VHTVPWDQLFRAPHQALLHTANR PEDECVCGRCDACHCARGCWDEPTQCVNCGPIR 536 417 VHTVPWDQLFRAPHQALLHTANR PEDECVCGRCDACHCARGCWDEPTQCVNCGPIR 536 417 VHTVPWDQLFRAPHQALLHTANR PEDECVCGRCDACHCARGCWDEPTQCVNCGPIR 536 417 VHTVPWDQLFRAPHQALLHTANR PEDECACGRCDACPTGCWDCGPTCCNCCHTRCF 536 537 GQBCVCEGRVACAPERSTVNGATCLPCHPECOPQNSTTCTGSEADQCVACAHYNDPPC 596 539 VARCPSGVKPDLSYMPTWRPDEGACQPCFINCTHSCTCTGSEADQCVACAHYNDPPC 596 539 VARCPSGVKPDLSYMPTWRPDEGACQPCFINCTHSCTCTGSEADQCVACAHYNDPRC 596 539 VARCPSGVKPDLSYMPTWRPDEGACQPCFINCTHSCTCTGSEADQCACAPHYNDPRC 596 539 VARCPSGVKPDLSYMPTWRPDEGACQPCFINCTHSCTCTGSEADQCACAPHYNDPRC 596 530 VARCPSGVKPDLSYMPTWRPDEGACQPCFINCTHSCTCTGSEADQCACAPHYNDPRC 596 531 TVGILLELINIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI   | SP GS        | 57 TSANIQEFAGCKKIFGSLAFLEBSFDGDPASNTAPLQBEQLQVFETLEBITGYLYISAWP 41.   | A, Molecule type: mRNA A, Residues: 1-1260 - BAR:> A, Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746 R; Masul, T.; Mann, A.M.: Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,   |
| 4.77 VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARCHCAGDGPTQCVNCSQPLR 536 4.77 VHTVPWDQLFRNHQALLHTANRPEDECVGEGLACHQCAGGPTQCVNCSHFR 536 4.77 VHTVPWDQLFRNHQALLHTANRPEDECVGEGLACHQCAGGPTQCVNCSHFR 536 5.37 GQECVEECRVAGGLPREVNARHCLPCHPECQPQNSTTCTGSEADCTACHTXDPPC 596 5.37 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDNGCPAACACHTXDPPC 596 5.37 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDNGCPAACACHTXDPPC 596 5.37 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDNGCPAACACHTXDPPC 596 5.37 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDNGCPAACACHTXDPPC 596 6.57 TVVGTLLVAVVGQLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVVGTLLFLJAVVGGLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVVGTLLFLJAVVGGLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVVGTLLFLJAVVGGLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVVGTLLFLJAVVGGLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVGTLLFLJAVVGGLTLTRRRQCTRYTTMRRLQCFTELVPPLTPSGAMPNQAPRILK 716 6.57 TVGTLLFLJAVVGGLTTRTRRQCTTRTTMRRLQCTTGTTTTTT 11  | oy<br>Ga     | DSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 47.  | Carcinogenesis 12, 19/3-19/8, 1991 A.Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no 2-thiazolyllformanide or N-methyl-N-nitrosourea. A.Reference number: A61204; MUID:92035293; PMID:1682063  |
| 537 GOECVECRVLOGLPREYVARACHCLPCHPECOPONGSVTCPCPEADQCVACAHYKDPPFC 596  537 GOECVECRWEGLPREYVARACHCLPCHPECOPONGSVTCPCPEADQCVACAHYKDPPFC 596  537 GOECVECRWEGLPREYVARCHCPCHPECOPONGSVTCPCBSBADQCACHTWBSPPC 596  597 VARCESGWKPDLSYMPTWKPDEEGACQPCPINCTHSCVDLDRGCCPAEQRASPLYSITA 656  597 VARCESGWKPDLSYMPTWKPDEEGACQPCPINCTHSCVDLDRGCCPAEQRASPLYSITA 656  657 TVVGILLPLYVLGVVLGVVGILIKRRQKIRKYTMRELLGFTELVPELTPSGAMFNQAQMRILK 716  717 TVGILLPLYTGVVLGVVGILIKRRQKIRKYTMRELLGFTELVPELTPSGAMFNQAQMRILK 716  718 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  719 TVGILLPLYTGVVGVGILIKRRQKIRKYTMRELLGFTELVPELTPSGAMFNQAQMRILK 716  710 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  711 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  712 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  713 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  714 FFELRKVKVLGSGARGTYYKGINIPOGENVK PVAIKVLRENTSPKANKEILDBAYVMG 776  715 LOSPYVSRLLGTCLTSTVQLVTQLMPYGCLLDHYREHGRAGSQDLLAWCVQLAKGMSYL 836  897 RRFTHQSDVWSYGTVWELMTFGAKPYDGTPAREILDIDFTSTYANGCRYPIKMTALESILR 896  897 RRFTHQSDVWSYGTVWELMTFGAKPYDGTPAREILDIDFTSTYRANGCRYPIKMTALESILR 896  897 RRFTHQSDVWSYGTVWELMTFGAKPYDGTPAREIPDDTFGSPLDDWGD 1016  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHHRHSSSTRSGGGDLTLGLEDDDMGD 1016  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHHRHSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHHRHSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHRHRSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHRHRSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYHRHRSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYTHRHRSSSTRSGGGGLTLGGRESEBPRSPLA 1076  1017 LVDAEEYLVPQQGFFPDDPAGAGAYTHRHRSSSTRSGGGGETLTGARFSBEADATGSPCRENCYCOLOGSPCPTORDLGMGAAKGLOSLPTHDPSPLQRYSSBDPTLPLTTGTVQVVDVPACQTFPCCPDDAGANGAYGOSTPTHPSPLQRYSSBDPTLPLTTGTVDVVDVPACQTFPCCPDDAGANGAYGOSTARRARPAGATGSCPTDTPTTGTVDVAPLTCSPC 1136  1017 PROGRAMMANGAYGGLENGARARPAGATLGARARPAGATLGSPCTUCTTGLEPSPCTDGTVAPLTTGTTOGTVAPLTTGTTOGTVAPLTTGTTOG | S S          | VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 53   | A;Accession: Acizua<br>A;Status: preliminary<br>A;Molecule type: DNA<br>A;Residues: 637-663,'V', 665-702 <mas></mas>  |
| 997 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656 597 VARCPSGVKPDLSYMPINKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPATSIIA 656 657 VARCPSGVKPDLSYMPINKYPDEEGACQPCPINCTHSCVDLDERGCPAEQRASPATSIIA 656 657 AVVGILLVVVLGVVPGILIKRRQQKIRKYTWRRLLQETELVBPLTPSGAMPNQAQMRILK 716 717 ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYWAG 776 717 VGSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 717 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 717 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 718 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVQTAKGWSYL 836 719 GSPYVSRLLGICLTSTVQLVTQLMPYCGLLDHYREHRGRLGSQDLIAWGVGTAYMINW 956 711 [  | දු පු        | GQECVEECRVLQGLPREYNNARHCLPCHPECQPQNGSVTCFGFBADQCVACAHYKDPPFC 59   | A;Note: authors translated the codon GCA for residue 25 as Val<br>C;Genetics:<br>A;Gene: neu<br>C;Superfamily: epidermal growth factor receptor; protein kinase homology  |
| 657 AVGILLIAVVLGVYFGILIKRRQOKIRKYTMRRLLQETELVEDLTPSGAMPNQAQMRILK 716 657 TVVGILLEPLVIGGVVYGILIKRRRQKIRKYTMRRLQETELVEDLTPSGAMPNQAQMRILK 716 657 TVVGILLEPLVIGGVVYGILIKRRRQKIRKYTMRRLQETELVEDLTPSGAMPNQAQMRILK 716 717 ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIRVLAENTSPKANKEILDEAYVMAG 776 717 VGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHVRENTGSPKANKEILDEAYVMAG 776 717 VGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHVRENRGRLGSQDLLAWCMQIAKGMSYL 836 817 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 818 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 819 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 810 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 811 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 812 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 813 EDVRLWHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 814 ENTHQSDWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMINV 956 815 KCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGSSFLDGPPYRSILEDDDMGD 1016 816  | è a          | 97 VARCPSGVKPDLSYMPIWKPPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 6   | C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorotein; phosphorotein; phosphoromain: signal sequence #status predicted <sig> F;1-19/Domain: signal sequence #status predicted <sig> F;20-1260/Product: protein-tyrosine kinase neu #status predicted <mat> F;658-680/Domain: transmembrane #status predicted <tmn></tmn></mat></sig></sig> |
| 717 ETELRKVKULGSGAFGTVYKGIMIPDGENVKIPVAIKVILRENTSPKANKEILDEAVYMAG 776 717 BTELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVILRENTSPKANKEILDEAVYMAG 776 718 GYPYVSRLIGICLTSTVOLVTQLMPYGCLLDHVRENRGRIGSQDLLNWCQIAKGMSYL 836 719 IGSPYVSRLIGICLTSTVOLVTQLMPYGCLLDHVRENRGRIGSQDLLNWCQIAKGMSYL 836 837 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 838 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILR 896 839 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEXHADGGKVPIKWALESILR 896 899 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 899 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 899 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 899 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 890 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 891 RFFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMV 956 892 RCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPSSELDSTFYRSLLEDDDMGD 1016 993 RCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPSSEEDEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVVHRRRSSSTRSGGGLTLGEPSEEERPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGLTLGEPSEEERPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGLTLGEPSEEERPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVHRHRSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGSTAHRRHSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVHRHRSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVHRHRSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVHRHRSSSTRSGGGCLTLGEPSEEEPRSPLA 1076 1017 LVDAEEYLVPQQGFFCPDPAPGAGGAVHRHRSSSTRSGGGCUTLGEPSEEPRSPLACSPQTALGEPSTGSPPTAPGAVAPLACSPQTAUFNFTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTU  | P &          | 57 AVVGILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILK 71.<br>   | F:723-988/Domain: protein kinase homology <kin> F:731-739/Region: protein kinase ATP-binding motif F:731,131,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted F:691/Binding site: phosphate (Thr) (covalent) #status predicted</kin>   |
| The transfer of the color of    | y d          | ETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG 77.<br>  | F;758/Active site: Lys #status predicted F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted Query Match 86.3%; Score 5876; DB 1; Length 1260;   |
|  | हे ह         | VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL 83   | Best Local Similarity 86.2%; Pred. No. 1.2e-232; Matches 1087; Conservative 54; Mismatches 110; Indels 10; Gaps 4   |
| BOYALVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEKHADGGKVPIRWIALBESILR   B96   09   | 3 &          | EDVRLVHRDLAARNVLVKSPINIVKITOFCLEDINKEHKGREGSQDEENWCVQIAARMISIE 83   | MELAAMCKWGLLALLEPGAASIQVCIFNNFIVSFWLKVFKNSASHLELYGGCQVV<br>   |
| 137 PEXVINGEDIGATE AND PRICE CONTINUED FOR PROPERTIES AND PROPER   | 8 &<br>8 &   | 7 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWIALESILR 89 7 RRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMV 95 | 57 QGNLELTYLFTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAV<br>   |
| 957 KCWIDSECRPRESSERRANDEDCREVENTINGUILLINGU | oy<br>Oy     | 97 KETHQSDVMSYGVTVMELMIFGHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT   | 117 LDNGDPLNNTTPVT-GASPGGLRELQLRSITEILKGGVLIQRNPQLCYQDTILWKDIFHK  |
| 1017 LVDAEEYLVPQQGFFFPDPAPGAGSTAHRAHRSSSTRSGGGELTLGMREPSGERPPRSPLA 1076  | g &          |   | 176 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDC  |
| 1077 PSEGAGSDVPOGLIGMGAAKGLQSLPTHDPSFLQRYZEDPTYPLPSETDGYVAPLTCSPQ 1136 1077 PSEGAGSDVPEGELGMGATKGPQSISPROLSPLQRYSEDPTLPLPTTLPPTTLPLPTTTLPTTLPTTLPTTLPTTLPTTLPTTTLPTTTLPTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTLPTTTTTT  | අ ර          |   | 236 CHBQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASC  |
|  | <b>3</b> 8 8 | UV. PERGASSUVEGGLGARGARGLQSEPTHUPSFLQRESEDETVPLESETUGYARLTCSPQ 11  11   | 240 CHEQCAAGCIGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASC 296 VTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRA 10  |

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Lee,

A.; Tam, A.W.;

A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray,

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A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression A;Reference number: A00641; MUID:84219729; PMID:6328312 A;Accession: A00641
                                                               A; Molecule type: mRNA
A; Residues: 1-1210 «ULL»
A; Residues: 1-1210 «ULL»
A; Residues: 1-1210 «ULL»
A; Cross-references: EMBL:X00588; NID:931113; PIDN:CAA25240.1; PID:9757924
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A;Residues: 1-29 <HA2>
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B;Haley, J.D.; Waterfield, M.D.
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A;Title: Contributory effects of de Novo transcription and premature tran
A;Reference number: A38672; MUID:91107677; PMID:1988448
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360 ITSDNVQEFDGCKKIFGSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYSLSAW
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A; Molecule type: DNA
A; Residues: 1-29 cHAL>
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A; Cross-references: Gs. M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A; Experimental source: carcinoma cell line A431-7
B; Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Me Rature 309, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs A; Reference number: A00642; MUID:84245835; PMID:6330563
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195,'M', 197,'A', 199-222,'S', 224-304,'RA', 307-32
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195,'M', 197,'A', 199-222,'S', 224-304,'RA', 307-32
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF rece
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I
Science 224, 843-848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplification
A; Reference number: A43615; MUID:84196372; PMID:6326261
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A;Residues: 713-964 «LIN»
A;Residues: 713-964 «LIN»
B;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley,
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
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A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183; PMID:6324343
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A;Residues: 25-30,'8',32-51;454-467 <WEB>
K;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleoti
A;Reference number: A60143; MUID:85182650; PMID:298
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A;Residues: 740-744,'X',746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen,
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epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Dates: Homo appiens (man) C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; A33

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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Gomment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Genetics: GB:G10613; OMIM:164870
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GB:120613; OMIM:164870
A;Introns: 25/1, 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorylation; duplication; glycoprotein; phosphorylation; extracellular duplication; glycoprotein; phosphorylation; extracellular domain repeat <EE1>F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <EXT>F;22-1255/Domain: EGF receptor extracellular domain repeat <EE1>F;325-605/Domain: EGF receptor extracellular domain repeat <EE2>F;365-605/Domain: EGF receptor extracellular domain repeat <EE2>F;365-605/Domain: protein kinase homology <KIN>F;726-734/Region: protein kinase homology <KIN>F;726-734/Region: protein kinase ATP-binding motif F;681/24,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (by autophosphorylation)
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protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C;Accession: A42562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 cARR-
A;Residues: 1-1260 cARR-
A;Residues: 1-1260 cARR-
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A;Residues: 1-1360 card-
A;Residues: 1-1360 card-
A;Reference Dimber: A61204; MUID:92035293; PMID:1682063
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PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI----I
                                                         TELKRROOKIRKYTMRRLLOETELVEPLTPSGAMPNOAOMRIL
                                                                                                                   SAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 637-663, V',665-702 <MAS>
A;Note: authors translated the codon GCA for residue 25 as Val
C;Genetics:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

July 22, 2003, 09:10:23; Search time 22.179 Seconds (without alignments) 5413.772 Million cell updates/sec

SEQ4-632-652-12 6796

1 MELAALCRWGLLLALLPPGA......1FKGTPTAENPEYLGLDVPV 1249 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f | protein-tyrosine k | protein-tyrosine k | epidermal growth f | rosine | kinase-related tra | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        | protein-tyrosine k | protein-tyrosine k |        | growth |        | protein-tyrosine k |         | insulin-like growt | insulin receptor p | insulin-like growt |
|-----------|---------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------------------|---------|--------------------|--------------------|--------------------|
| SUMMARIES | ID            | A24571             | TVRTNU             | 148161            | GQHUE              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV             | TVYUH              | GQFFE              | S35745 | S00727             | B44776             | TVFVEB             | A36325             | E88257 | S70712             | S70713             | A45558 | A42032 | A27131 | S13807             | \$13808 | T43220             | INHUR              | T43212             |
|           | DB            | Н                  | -                  | 7                 | 7                  | ~      | н      | 7      | н      | 7                  | 7                  | п                  | ч                  | н                  | ~      | ~                  | ~                  | н                  | ~                  | N      | N                  | ~                  | -      | N      | N      | N                  | ~       | N                  | н                  | N                  |
|           | Length        | 1255               | 1260               | 1254              | 1210               | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698                | 604                | 1330               | 544    | 545                | 540                | 540                | 644                | 1323   | 1374               | 1369               | 1717   | 527    | . 843  | 346                | 311     | 1363               | 1382               | 1607               |
| æ         | Query         | 97.4               | 86.2               | 85.8              | 45.8               | 45.4   | 44.9   | 43.0   | 38.8   | 35.3               | 33.8               | . 25.4             | 24.4               | 23.8               |        | 23.5               | 23.2               | 23.2               | 22.2               | 18.9   | 18.9               | 17.5               | 16.9   |        | 14.4   | 11.9               | 11.1    | 10.5               | 10.0               | 10.0               |
|           | Score         | 6619               | 5860               | 5833.5            | 3115               | 3082   | 3051.5 | 2925.5 | 2635   | 2398.5             | 2297.5             | 1723.5             | 1660               | 1617.5             | 1604   | 1597               | 1580               | 1578               | 1509               | 1282   | 1282               | 1190               | 1148   | 1126   | 975.5  | 806.5              | 754.5   | -                  | 681                | 619                |
|           | Result<br>No. | н                  | 8                  | e                 | 4                  | w      | 9      | 7      | æ      | σ                  | 10                 | 11                 | 12                 | 13                 | 14     | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22     | 23     | 24     |                    | 26      | 27                 | 28                 | 29                 |

| insulin receptor p | insulin receptor-r | insulin receptor p | protein-tyrosine k | insulin receptor-r | insulin-like growt | insulin receptor - | insulin-like growt | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A36080             | A36502             | A34157             | T18534             | B36502             | IGHUR1             | A56081             | A33837             | T30346             | S57245             | 833596             | A45388             | 150612             | 805582             | JC4200             | A39753             |
| N                  | ~                  | ~                  | 7                  | 7                  | Н                  | н                  | ~                  | N                  | ~                  | ~                  | ~                  | ~                  | Н                  | ~                  | N                  |
| 1383               | 1300               | 1372               | 1477               | 1268               | 1367               | 2148               | 1371               | 1390               | 2101               | 1001               | 1028               | 952                | 1114               | 1052               | 984                |
| 10.0               | 10.0               | 10.0               | 6.6                | 9.7                | 9.3                | 9.1                | 9.1                | 9.0                | 9.0                | 9.8                | 9.8                | 8.5                | 8.5                | 8.5                | 8.5                |
| 678                | 677.5              | 677.5              | 673                | 099                | 632                | 618.5              | 617                | 615                | 612                | 584.5              | 581.5              | 576.5              | 576                | 575                | 574.5              |
| 30                 | 31                 | 32                 | 33                 | 34                 | 32                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

RESULT 1

|   | A24571   |
|---|--|
|   | protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human                             |
|   | N, Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB  |
|   | C;Species: Homo sapiens (man)  |
|   | C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999                |
|   | C;Accession: A24571; A25491; A44188; B44188; I59509; I57622                                |
|   | R; Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;   |
|   | Nature 319, 230-234, 1986  |
|   | A, Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f. |
|   | A;Reference number: A24571; MUID:86118663; PMID:3003577                                    |
|   | A;Accession: A24571  |
|   | A; Molecule type: mRNA   |
| - | A;Residues: 1-1255 <yam></yam>   |
|   | A; Cross-references: GB:X03363; NID:q31197; PIDN:CAA27060.1; PID:q31198                    |
| _ | R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.                                       |
|   | Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985  |
|   | A; Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm  |
|   | A.Doforonce mimber. A26401. MITD. 06616720. DMTD. 2006067                                  |

A;Reference number: A25491; MUID:86016729; PMID:2995967

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P Science 230, 1132-1139, 1985

receptor shares chromose A;Title: Tyrosine kinase receptor with extensive homology to EGF A;Reference number: A44188; MUID:86070181; PMID:2999974

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 832-909 <REX>
A;Cross-references: GB:L29395; NID:9459807; PIDN:AAA35809.1; PID:9459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu) Promoter: evidence for multiple mechanisms for transcriptional
A;Reference number: I57622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL>

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1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
                                                                                                                                                                                                                                                      1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1169
                                                                                                                         58 GLEGCP---NGSKTPSIAAGVVGGLICLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 113
                                                            817 LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 876
                                                                                                                                                                                                                                  VEPLTPSGAMPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756
                                      638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRILQETEL 696
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Search completed: July 22, 2003, 09:10:12 Job time : 31.9062 secs

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                                                                                                                                                                    294 YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE
  578 GPEADQCVACAHYKDPPFCVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDL
                                                                                                            GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLOEREL
                                                                                                                                                                                                                                                        ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
                          638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
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54.3%; Pred. No. 2.8e-59;
iive 69; Mismatches 126;
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S,Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: aTP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;135-400/Domain: protein kinase homology «KIN»
F;143-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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    procein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus cipacise: avian erythroblastosis virus cipate: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745 A;Reference number: S35743 A;Reference number: S35743 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference number: S35745 A;Reference
                                                                                                                                           LVVVLGVVFGI-LIKRRQOKIRKYT--MRRLLQETELVEPLTPSGAMPNQAQMRILKETE
                                                                                    PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
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23.8%; Score 1617; DB 2; Length 544;
Best Local Similarity 54.3%; Pred. No. 1.5e-59;
Matches 341; Conservative 70; Mismatches 125; Indels 9;
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A;Readudes: 'Ay', 832-866,'V',868-943,'QTDSLVK' <WAD>
A;Readudes: 'Ay', 832-866,'V', 868-943,'QTDSLVK' <WAD>
A;Cross-references: EMBL.X02293; NID:97922; PIDN:CAA26157.1; PID:9929565
C;Comment: This sequence is tentative because the introns have not been identified.
C;Genetics:
A;Gene: FlyBase:Egfr
A;Cross-references: FlyBase:FBgn0003731
A;Map position: 2 57F
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor specificed <EXTO-C;Superfamily: epidermal growth factor specificed <EXTO-F;733-764/Domain: transmembrane #status predicted <TMM>F;1-732/Domain: intracellular #status predicted <INM>F;816-824/Region: protein kinase homology <INN>F;816-824/Region: protein kinase homology <INN>F;816-824/Region: protein kinase ATP-binding motif F;122,300,324,363,518,688,695,700/Binding site: carbohydrate (Asn) (covalent) #status predicted F;843/Active site: Lys #status predicted F;843/Active site: Lys #status predicted F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
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NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C.Species: Drosophila melanogaster
C.Species: 17-Mar.1987 #sequence_revision 17-Mar.1987 #text_change 11-Jun-1999
C.Species: 17-Mar.1987 #sequence_revision 17-Mar.1987 #text_change 11-Jun-1999
R.Livneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Cell 40, 599-607, 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding
A;Accession: A00640
A;Accession: A00640
A;Molecule type: DNA
A;Reference number: BMBL:KO3054
R;Waddworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature-314, 178-180, 1985
A;Title: A Drosophila genomic sequence with homology to human epidermal growth factor re
A;Reference number: A38021; MUID:85137938; PMID:2983232
A;Accession: A38021
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                                                                          587 CAHYKDPPFCVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                       RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                        Gaps
                                      126;
                                      Indels
24.8%; Score 1688; DB 1; L
51.7%; Pred. No. 2e-62;
ive 76; Mismatches 131;
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| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172    | Qy 697 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756 | Oy 757 ENTSPRANKEILDEAVVWAGVGSPYVSRLIGICLISTVQLVTOLMPYGCLLDHVRENRGR 816 | Qy 817 LGSQDLIAWGWQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 876  | Qy 877 YHADGGKVPIKWMALESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLE 936   | Qy 937 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQ-NEDLG 995   | Qy 996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDFAPGAGGWVHHRHRSSSTRSG 1055   | Qy 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110 | QY         1111 RYSEDPTVPLPSET DGYVAPLTCSPQPEYUNQPDVRPQPPSPREGPLPAARPAGATLE 1168 |   |   |  | A;Nolecule type: DNA A;Nolecule type: DNA A;Nolecule type: DNA A;Residues: 1-604 <yam> A;Residues: 1-604 <yam> A;Residues: GB:KOl216; NID:g209676; PIDN:AAA42400.1; PID:g209678 A;Cross-references (GB:KOl216; NID:g209676; G.; Claverie, J.M.; Saule, S.; Martin, S;Sance 224, 1456-1459, 1984 A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of A;Reference number: A38022; MUID:84223957; PMID:6328658 A;Accession: A38022</yam></yam>  | A;Wolecule type: DNA<br>A;Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 <deb><br/>A;Cross-references: GB:K02006<br/>C;Genetics:</deb> | A;Gene: erbB<br>C;Superfamily: epidermal growth factor receptor; protein kinase homology<br>C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specifi;<br>F;130-395/Domain: protein kinase homology <kin><br/>F;138-146/Region: protein kinase ATP-binding motif<br/>F;165/Active site: Lys #status predicted</kin> |
|---|---|---|--|---|---|--|--|--|---|---|--|--|---|---|
| DD 755 TDHMLAVGSLDHAHIVRLIGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGV 814 | QY 828 QIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIK 887 | OY 888 WMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPIC 947 | QY 948 TIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVJQNEDLGPASPLDSTFYRS 1007 | QY 1008 LLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSE 1067 | QY 1068 EEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQ 1099  1018 EGLATSLGSALSLPTGTLTRPRGSGSLLSPSSGYMPMNQSSLGEACLDSAVLGGREQFSR 1077 | OY 1100 SLPTHDPSFLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY 1139  1078 PISLH-PIPRGRPASESSEGHVTGSEAELQEKVSVCRSRSRSRSPRPRGDSAY 1129 | OY 1140 UNOPDVRPOPPSPREGP  | OY 1182 KDVFAFGGAVENPEXLTPGGGAAPOPHPP 1210  Db 1190 EDEEVEYMNRKRRGSP-PRPP 1209   | LT 11<br>LV ein-t<br>ntain<br>ecies<br>te: 3<br>cessi | Cell 41, 719-726, 1985 A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A;Reference number: A00643; MUID:85228222; PMID:2988784 A;Accession: B00643 A;Accession: B10643 A;Melecule type: mRNA A;Residues: 1-698 <nil></nil> | A;Cross-references: GB.Mi0066; GB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g211750 A;Note: in Genbank entry CHKERBBF, release 109.0, the source is designated as Gallus gal C;Comment: This protein is synthesized as a gag-env-erbB protein. | C, Superfamily: epidermal growth factor receptor; protein kinase homology C, Superfamily: epidermal growth factor receptor; protein kinase homology C, Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p C, Keywords: ATP; oncogene; fisherment factors of constant of constant of the co | Query Match<br>Best Local Similarity 51.7%; Pred. No. 2.4e-64;<br>Matches 370; Conservative 80; Mismatches 141; Indels 125; Gaps 18;      | QY         578 GPEADQCVACAHYKDPPFCVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDL 637           I   |

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ESSEGHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLSPPGLEEE 1154
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VFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNW
                               DQLFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                                 EECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                            THCNFLNGEPREPAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                                                                        QYIKANSKFIG----ITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTS
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NyAlternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 1
C;Accession: JC4387
E;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, Gene 155, 279-284 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of th A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Accession: JC4387
A;Molecule type: mRNA
A;Residues: A:1339 <HEL>
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A; Experimental source: liver
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A; Experimental source: liver
C; Coment: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
C; Comment: This protein is a functional heregulin receptor that transduces signals to th
C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoloc
C; Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein
F; 1-19/Domain: signal sequence #status predicted <AMA>
F; 1-19/Domain: signal sequence #status predicted <AMA>
F; 06-07/Domain: protein kinase homology <AMA>
F; 106-97/Domain: protein kinase homology <AMA>
F; 106-97/Domain: protein kinase homology <AMA>
F; 106-97/Domain: protein kinase ATP-binding motif
F; 106-107/Domain: protein kinase ATP-binding motif
F; 106-107/L156, 1194, 1196, 1219, 1257, 1259, 1273, 1286, 1325/Binding site: phosphate (Tyr) (c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LNYNT----NSSHALRQLKFTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAEIVVKÁNGANCPPCHEVCKG-RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHHSLNWTRLILRGPSEERLDIKYDRPLGECLAEGKVCDPLCSSGGCWGPAPGQCLSCRNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGL--GMQYIKANSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVHTVPWDQLIFRNPHQALLHTA-NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCVARCPQYIKANSKFIG----ITELPDEEGACQPCPINCTHSC--VDLDDKGCPAEQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMP
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                                                                                                                                                                                                                                                                                                                                                            3 LAALCRWGLLIJALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
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                                                                                                                                                                                                                                                                                 Query Match 33.9%; Score 2304.5; DB 2; Length 1339; Best Local Similarity 40.4%; Pred. No. 2.4e-87; Matches 521; Conservative 169; Mismatches 432; Indels 167;
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seq4-579-593-12.rpr

| ON 1243 ARNDRVIG 1250  | 1149 AENLEYLG 115  | RESULT 9 A36223 kinase-related transforming protein (erbB3) (EC 2    | C;Species: Homo sapiens (man) C;Date: 04-Oct-1991 #sequence_revision 13-Jan-199 C;Accession: A36222; 159164 R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C | Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989 A,Title: Isolation and characterization of ERBB3, A,Reference number: A36223; MUID:90083234; PMID:2 A,Accession: A36223 | A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1342 <kra> A;Cross-references: GB:M29366</kra>  | R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; G<br>Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990<br>A;Title: Molecular cloning and expression of anot<br>A;Reference number: I59164; MUID:90311312; PMID:2 | A;Accession: IS9164 A;Status: preliminary; translated from GB/EMBL/DD A;MOlecule type: mRNA A;Residues: 1-559, G', 561-957, 'F', 959-1063, 'G', 10 | A;Cross-references: GB:M34309; NID:g183990; PIDN:<br>Cgenetics: A;Genetics: A;Cross-references: GDB:119880; OMIM:190151 | A,Map position: 12q13-12q13 C,Superfamily: unassigned Ser/Thr or Tyr-specific p: C,Keywords: ATP; phosphotransferase F;707-972/Domain: protein kinase homology <kin></kin> | P://15-723/Region: protein Kinase ATP-binding motif<br>Query Match 35.1%; Score 2388.5; DB<br>Best Local Similarity 40.1%; Pred. No. 8.8e-91 | rd<br>E  |  | 128   | 126<br>188   | 179  | 238  | 297  | DD 351 FVNCTKILGANLDFLITGENGDFWHKIPALDPEKLNVFF<br>QY 424 VFQNLQVIRGRILHNGAVS-LTLQGLGISWLGLRSLRI<br> |
|--|--|--|---|---|---|--|--|---|--|--|--|--|---|--|--|--|--|---|
| 123 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP 179 | 180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238 | 239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298 | 299 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358  10  | 359 ITEL-EFAGCKKIFGSLAFLPBSFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPD 417<br>  :   | 418 SLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 ::                 :           :   : | 477 VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 536 1   | 537 GOECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPPC 596   | 597 VARCPQYIKANSKFIGITELPDEGGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656 :  | 657 AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRILQGTBLVBPLTPSGAMPNQAQMRILK 716<br>   | 717 ETELRKUKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG 776<br>   | 777 VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL 836<br> | 837 EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIIR 896<br> | 897 RRFTHQSDVWSYGVTVWELWTFGAKBYDGIBAREIPDLEKGERLPQPPICTIDVYMIMV 956<br> | 957 KCWMIDSECRPRFRELVSEFSRMARDPQRFVVJQNEDLGPASPLDSTFYRSLLEDDDDMGD 1016<br> | 1017 LVDAEEYLVPQGGFFCPDFAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076<br> | 1077 PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVAPLTCSP 1135 | 1136 QPEYVNQPDVRPQPPSPREGPLP-AARPAGATLERAKTLSPGKNGVVK 1182<br>       <br>  1 | 1183 DVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPFSTFKGTPT 1242<br>                          |
| q  | & B  | රු පු  | è 9   | δ d   | \$ B  | <i>&amp;</i> ₽   | \$ g   | & g   | <i>∂</i> 8   | & g  | Qy<br>Dp   | δ g  | & g   | ò 8  | ò 9  | o<br>P   | ò a  | & q   |

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a third member of the ERBB/epidermal g
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52; Indels 143; Gaps 35;
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                      #text_change 17-Nov-2000
7.1.-) precursor - human
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AAA35979.1; PID:g306841
                                                                                                                                                                                                                                                                                                                                                               )B 2; Length 1342;
                                            ; Aaronson, S.A.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

| July 22, 2003<br>SEQ4-5-25-12<br>6774<br>I MELAALCRWGL | July 22, 2003, 08:11:38 ; Search time 37.7958 Seconds (without alignments) 4403.399 Million cell updates/sec | SEQ4-5-25-12<br>6774<br>1 MELAALCRWGLILALLPPGATFKGTPTAENPEYLGLDVPV 1249 |
|--|--|---|
|  | 7 22, 2003,  | 4-5-25-12<br>4<br>ELAALCRWGLL   |
|  | Run on:  | Title:<br>Perfect score:<br>Sequence:                                   |

| SEQ4-5-25-12 : 6774 1 MELAALCRWGLLLALLPPGATFKGTPTAENPEYLGLDVPV 1249 | :: BLOSUM62<br>Gapop 10.0 , Gapext 0.5 | 908470 segs, 133250620 residues | Total number of hits satisfying chosen parameters: 908470 |
|---|--|---------------------------------|---|
| Title:<br>Perfect score:<br>Sequence:                               | Scoring table: BLOSUM62<br>Gapop 10    | Searched:                       | Total number  |

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|--|--|---|
| TOTAL HUMBEL OF HITE SACISTAMS CHOSEN PARAMETERS | Minimum DB seq length: 0<br>Maximum DB seq length: 200000000 | Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries |

| A Geneseq 101002:*<br>1: /SIDS2/gcgdata/geneseq/genesecp-embl/AA1980.DAT:* | 2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* | 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* | 4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* | 5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:* | 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:* | 7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* | 8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* | 9: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:* | <pre>10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*</pre> | <pre>12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*</pre> | <pre>13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*</pre> | 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:* | <pre>15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*</pre> | <pre>16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*</pre> | 17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* | <pre>18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*</pre> | 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:* | <pre>21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*</pre> | <pre>22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*</pre> | 23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* |  |
|--|--|--|--|--|--|--|--|--|--|--|--|---|--|--|---|--|---|--|--|---|--|
| Database :   |  |  |  |  |  |  |  |  |  |  |  |   |  |  |   |  |   |  |  |   |  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            |   |        | Description          | Human herequlin 2 | Human tyrosine kin | HER2 transgene pla | Human HER2 (ErbB2) | HER-2/neu protein. | Human HER-2/neu on | Human HER-2/neu pr | Amino acid sequenc | Human HER-2/neu pr | HER2/neu amino aci |
|------------|---|--------|----------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| COLUMNITOS |   |        | ID                   |                   | AAE12130           | AAB60167           | AAU74545           | AAW01111           | AAW92406           | AAB21198           | AAY84780           | AAB85458           | AAG88267           |
|            |   |        | DB                   | 21                | 22                 | 22                 | 23                 | 17                 | 20                 | 21                 | 21                 | 22                 | 22                 |
|            |   |        | re Match Length DB 1 | 1255              | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               |
|            | ф | Query  | Match                | 98.6              | 98.6               | 98.6               | 98.6               | 98.5               | 98.5               | 98.5               | 98.5               | 98.5               | 98.5               |
|            |   |        | Score                | 6678              | 6678               | 6678               | 6678               | 6672               | 6672               | 6672               | 6672               | 6672               | 6672               |
|            |   | Result | No.                  |                   | 7                  | m                  | 4                  | ß                  | 9                  | 7                  | <b>6</b> 0         | σ                  | 10                 |

| =        | 7         | σ         | 1255                                    | 2   | AAE24067   | Human Her-2 protei |
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| 4.       | 6677      |           | 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 3 6 | 1.5        | Her-2/neu          |
|          | 2         | 9.2       | 1433                                    | 4   | 55         | nce of             |
| 16       | 5.5       | 96        | 1223                                    | 23  | 392        | east can           |
| 17       | 35        | 93        | 1200                                    | 21  | 120        | Human HER-2/neu pr |
| 18       | 864.      | 86.       | 1256                                    | 21  | AAB21199   | Rat HER-2/neu prot |
| 19       | 864.      | 86.       | 1256                                    | 23  | AAM51144   | Rat Her-2/neu onco |
| 20       | 6         | 86.       | 1256                                    | 21  | AAB21206   | Mouse Her-2/neu pr |
| 21       | 839.      | 86.       | 1256                                    | 22  | AAG62860   | Amino acid sequenc |
| 22       | 839.      | 86.       | 1256                                    | 23  | AAM51151   | Mouse Her-2/neu on |
| 23       | 75        | 70.       | 919                                     | 21  | AAB21203   | Human HER-2/neu fu |
| 24       | 75        | 70.       | 919                                     | 23  | AAM51148   | Her-2/neu extracel |
| 25       | 89.       | 58.       | 920                                     | 23  | AAM51152   | 2/nen              |
| 26       | 989.      | . 58      | 926                                     | 23  | AAM51153   |                    |
| 27       | 64        | 53.       | 712                                     | 21  | AAB21204   | Human HER-2/neu fu |
| 28       | 64        | 53.       | 712                                     | 23  | AAM51149   | Her-2/neu extracel |
| 29       | 49        | 51.       | 782                                     | 18  | AAW19764   | Her2-GM-CSF immuno |
| 30       | 49        | 51.       | 653                                     | 21  | AAB21200   | Extracellular HER- |
| 31       | 49        | 51.       | 653                                     | 23  | AAM51145   | Human Her-2/neu on |
| 32       | 45        | 51.       | 645                                     | 22  | AAB60408   | Human ErbB2 oncopr |
| 33       | 45        | 51.       | 645                                     | 22  | AAB61593   | Human ErbB2 extrac |
| 34       | 39        | 50.       | 951                                     | 21  | AAY44993   | DC8scFv-erbB2EC fu |
| 35       | 28        | 48.       | 624                                     | 11  | AAR08222   | Extracellular port |
| 36       | 13        | 46.       | 1210                                    | 21  | 25         | Amino acid sequenc |
| 37       | 13        | 46.       | 1210                                    | 21  | 190        | cepto              |
| 38       | 13        | 46.       | 1210                                    | 23  | 301        |                    |
| 39       | 13        | 46.       | 1210                                    | 23  | 976        | epide              |
| 40       | 13        | 46.       | 1210                                    | 22  | 342        | acid sequen        |
| 41       | 60        | 45.       | 1210                                    | 23  | ABP51768   | Human epidermal gr |
| 42       | 08        | 45.       | 583                                     | 23  | 148        | ္ဌ                 |
| 43       | 9         | 45.       | 587                                     | 23  | 048        | щ                  |
| 44       | 9         | 45.       | 589                                     | 23  | $^{\circ}$ |                    |
| 45       | 08        | 45.       | 009                                     | 23  | 048        | ein f              |
|          |           |           |   |     |            |                    |
|          |           |           |   |     | ALIGNMENTS |                    |
|          |           |           |   |     |            |                    |
| RESULT 1 | н         |           |   |     |            |                    |
| 4        | AAY92620  | standard; | Protein;                                |     | 1255 AA.   |                    |
|          |           |           |   |     |            |                    |
| AC AP    | AAY92620; |           |   |     |            |                    |

|                      | AAY92620 standard; Protein; 1255 AA. |   | ;·(       | × | 10-AUG-2000 (first entry) |   | Human heregulin 2 (Her2). |   | Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; | self-protein; cancer; breast cancer; prostate cancer; | sociated peptide antigen; foreign epitope. |   | oiens.        |   | Location/Qualifiers | 1173   | /label= N-terminal | <pre>/note= "mature polypeptide"</pre> | 525    | /label= insertion_region | /note= "suitable For foreign epitope insertion" | 5973   | /label= insertion region | /note= "suitable for foreign epitope insertion" | 103117 | /label= insertion_region | /note= "suitable for foreign epitope insertion" | 149.163 | /label= insertion region<br>/nore= "en:table For foreign en:tone insertion" | / more- bureaute for totergin epicope misercion 174323 |  |
|----------------------|--------------------------------------|---|-----------|---|---------------------------|---|---------------------------|---|--|---|--|---|---------------|---|---------------------|--------|--------------------|--|--------|--------------------------|---|--------|--------------------------|---|--------|--------------------------|---|---------|---|--|--|
| RESULT 1<br>AAY92620 | AAY92620 8                           |   | AAY92620; |   | 10-AUG-20                 |   | Human here                |   | Heregulin  | self-prot   | cell-asso                                  |   | Homo sapiens. |   | Key                 | Domain |                    |  | Region | ,                        |   | Region |                          |   | Region |                          |   | Region  |   | Domain   |  |
| AAYS                 | ΩÏ                                   | × | AC        | × | DŢ                        | × | DE                        | × | ₹  | Κ   | ₹.   | × | os            | × | H                   | FT     | FT                 | FT                                     | FT     | FT                       | FT  | ΕŢ     | ŁΤ                       | FT  | FT     | FΤ                       | ĽЧ  | Н       | FF  | I I  |  |

seq4-5-25-12.rag

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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and Cytteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suiteable for the insertion of foreign T helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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/note= "suitable for foreign epitope insertion"
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'label = Cysteine_rich_domain
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3irk P, Karlsson G;
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (Self-proteins), e.g. human prostate specific membrane antigen (PSM) thereguln 2 (Herz) and/or fibroblast growth factor 8b (FGFBb). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Herz and human/murine FGFBb comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer
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                                                                                                                                                                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                  HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
                                                                                                                                                                                                                                        GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1249
                                                                                                                                                                                                                                                                                                                                                                         antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunotherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                                                 GGAAPQPHPPPAESPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                                                                                                                                                                    complex; vaccine;
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                                                                                                         The internation learness to symmetric the composition of the complex (MHC) molecules and enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCS), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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ive 4; Mismatches
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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               YVSRLGGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGMSYLEDVR
                                                                                                                                       LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
                                                                                                                    LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                                                                                              HOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWM
                                                                                                                                                                                                                                                                                                   EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                                                                                                                                                                                                                                                                                                      NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                         YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQLAKGMSYLEDVR
                                                                                                                                                                                                                                                                                                                                                             AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;
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N-PSDB; AAF24297.
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is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating enuronal, gliah, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, anglogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovar stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; BrbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; estrocytal disorder; inflammatory disorder; anglogenic disorder; inflammatory disorder;
          LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                       Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The product of early and the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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the HER-2/neu oncogene is
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901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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                             HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLJEKGERLPQPPICTIDVYMIMVKCWM
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/note= "region which elicits
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93US-0033644.
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N-PSDB; AAX01912.
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31-MAR-1995;
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120 180 240 300 DESVEONLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480 114 174 294 354 360 414 420 540 600 9 of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence. 474 534 594 654 714 720 774 780 834 894 9 IQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEETTGYLYISAWPDSLP ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC ILLVVVLGVVFGILIKRROOKIRKYTMRRLLOETELVEPLTPSGAMPNOAOMRILKETEL LTLIDTNRSHACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC **AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP** IQEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL RKVKVLGSGA=GTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 1 MELAALCRWGLLLALLPPGAASTQVCT-----QYIKANSKFIGITELLYQGCQVVQGNL DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV RKVKVLGSGA:GTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP YVSRILGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR YVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC Gaps . 9 Length 1255; Indels

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Pred. No. 0;
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98.2%;
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Best Local Similarity 98.2
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                                                                                                                                                                                                                  NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
                                                                                                                                                                                                                                   The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by aliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                   IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                          EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                                              AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                                                                                                                     HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
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                                                                                                                                                                  GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1249
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 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                                                                                                                                                MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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larity 98.2%; Pred. No. 0;
Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is clulture in vitro and binds to a complex of an epitope (I), bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino caids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (II) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for inducing cellular immune response for the correction and treatment of cancer. (I) and (III) are useful for inducing cellular immune response to a tumour-associated antigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte sample form a patient and catecting the presence of bound T lymphocyte sample form a patient of in whole antigens may be avoided. Selected epitopes may be present in whole antigens may be avoided. Selected epitopes may be combined to chhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the apportunity to combine epitopes derived from vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-cumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88126 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
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cancer -
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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Length 1255;

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Query Match

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                        61 ELTYLPTNASLSFLØDIØEVØGYVLIAHNOVROVPLØRLRIVRGTØLFEDNYALAVLDNG
                                                                                              DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKANQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                              1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                           NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                    AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                  GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a human patient. The invention is useful for stimulating a r cell response in a human patient as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a polypeptide in appropriate host cells. The composition is useful in propriet or the reatment of cancer, prophylactic or the reatment of cancer.
Her-2/Neu protein; immune response; gene therapy; breast cancer; leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                    /note= "Naturally processed HLA-B44-restricted epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferably for the immunotherapy of breast cancer and other Her-2/Neu-associated malignancies. The invention is useful in gene therapy. The
                                                   Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
                                     GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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1021..1030
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                                                                                                                                     (first entry)
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Query Match

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                                                                                                           1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines
                              AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                          NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                       1249
                                                                                                                                                                       Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain
                                                                                                                                                                                                                                                                                                                                                                                       Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185; tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                                                                                                                                          Human Her-2/neu oncogene-encoded p185 glycoprotein.
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/note= "extracellular domain"
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of a hosphorylation domain (or its Delteap fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
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The invention relates to a method for innibiting develupment of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polymucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic myelogenous leukaemia (CML), myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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Best Local Similarity 98.2%;
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                                                                                                                                                                                                                                                                                                                                                          AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILRRRFT
                                                                                                                                                     HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWM
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                                                                   LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                                                       DVYMIMVKCWM
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLI
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904
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IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                                                           GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1249
                                                                                                                                                                                                                     c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. actidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). X in AAR39583 represents the location of a stop codon in AAQ46083.
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Pred. No. 0;
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N-PSDB; AAQ46083.
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                                                   ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                     DPLNNTTPVTGAS PGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI PHKNNQLA
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                            LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                           AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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GenCore version 5.1.6
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protein search, using sw model OM protein

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec Run on:

SEQ4-59-73-12 6809 1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1255 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| •         | цo             | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f | >      | protein-tyrosine k | epidermal growth f | protein-tyrosine k | kinase-related tra | protein-tyrosine k | protein-tyrosine k | epidermal growth f | w      | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        |        | ~      | protein-tyrosine k | insulin-like growt | insulin receptor p | insulin receptor p |
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| SUMMARIES | ΩI             | A24571             | TVRTNU             | 148161            | GOHUE              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV | TVYUH              | GOFFE              | S35745             | 800727             | B44776             | TVFVEB             | A36325             | E88257 | 870712             | S70713             | A45558             | A42032 | A27131 | S13807 | S13808             | T43220             | INHUR              | A36080             |
|           | BB             | 7                  | •                  | •                 | Н                  | •      | Н      | •      |        | N                  | ~                  | Н      | 7                  | ٦                  | ~                  |                    |                    | Н                  |                    |        | N                  |                    |                    |        |        |        | 7                  |                    |                    |                    |
|           | Length         | 1255               | 1260               | 1254              | 1210               | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698    | 604                | 1330               | 544                | 545                | 540                | 540                | 644                | 1323   | 1374               | 1369               | 1717               | 527    | 843    | 346    | 311                | 1363               | 1382               | 1383               |
| dŧ        | Query<br>Match | 98.8               | 86.9               | 86.9              | 45.8               | 45.4   | 45.3   | 43.3   | 39.0   | 35.1               | 34.0               | 25.9   | 25.0               | 4.                 | 24.2               | 4.                 | 23.8               | ë.                 | 21.8               | 18.7   | 18.7               | 17.4               | 16.8               | 16.4   |        | 11.8   | 11.1               |                    | 10.5               | 10.4               |
|           | Score          | 6729               | 5919               | 5918.5            | 3117               | 3093   | 3085.5 | 2950.5 | 2653   | 2389.5             | 2316.5             | 1766.5 | 1703               | 1654.5             | 1647               | 1640               | 1623               | 1621               | 1485               | 1275   | 1275               | 1187               | 1146               | 1117   | 955.5  | 806.5  | 754.5              | 742                | 717                | 710                |
|           | Result<br>No.  | -                  | 73                 | Э                 | 4                  | S      | 9      | 7      | 89     | δ                  | 10                 | 11     | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22                 | 23     |        |        |                    |                    | 28                 | 29                 |

| insulin receptor p | insulin-like growc<br>insulin receptor-r | insulin receptor-r | protein-tyrosine k | insulin-like growt | insulin-like growt | insulin receptor - | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | tyrosine kinase Mp | protein-tyrosine k | mouse developmenta | protein-tyrosine k |
|--------------------|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A34157             | T43212<br>A36502                         | B36502             | T18534             | IGHUR1             | A33837             | T30346             | A56081             | S57245             | A54092             | 150612             | S49004             | S05582             | 148652             | 833596             |
| 00 0               | 7 7                                      | N                  | ~                  | Н                  | N                  | N                  | Н                  | N                  | ď                  | 0                  | 7                  | Н                  | 7                  | 0                  |
| 1372               | 1300                                     | 1268               | 1477               | 1367               | 1371               | 1390               | 2148               | 2101               | 987                | 952                | 977                | 1114               | 987                | 1001               |
| 10.4               | 10.3                                     | 9.9                | 9.9                | 9.6                | 9.4                | 9.3                | 9.1                | 9.0                | 9.0                | 8.7                | 8.7                | 9.8                | 8.6                | 9.8                |
| 709.5              | 688.5                                    | 919                | 672                | 653                | 642                | 635                | 618.5              | 613                | 610                | 591.5              | 589.5              | 588                | 586                | 586                |
| 30                 | 32<br>32                                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB;

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999
C;Accession: A24571; A24591; A44188; B44188; I59509; I57622
C;Accession: A24571; A2491; A44188; B44188; I59509; I57622
R;Yanmanoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; 7
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f. A;Reference number: A24571; MUID:86118663; PMID:3003577

A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. US.A. 82, 6497-6551, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermana A;Reference number: A25491; MUID:86016729; PMID:2995967

A;Accession: A25491
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 737-1031 ASBNA
A;Rosidues: 737-1031 ASBNA
A;Rosidues: 737-1031 ASBNA
A;Cross-references: GB:Mi1767; NID:g182163; PIDN:AAA35808.1; PID:g553282
A;Cross-references: GB:Mi1767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Crossens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P
A;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
A;Reference number: A44188; MUID:86070181; PMID:2999974

A; Accession: A44188
A; Molecule type: DNA
A; Residues: 740-910 < COU1.>
A; Molecule type: DNA
A; Cross-references: GB:M1.2036; NID:g183988; PIDN:AAA35978.1; PID:g183989
A; Accession: B44188
A; Molecule type: mRNA
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A;Residues: 832-909 <REX>
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B;Tal. M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A;Reference number: IS7622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL> A; Accession: I57622

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720 720 780 780 840 840 900

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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho:
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
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A; Creatidues: 1-1260 <BAR
A; Creatinogenesis: 12, 1975-1978, 1991
Carcinogenesis: 12, 1975-1978, 1991
A; Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no 12-thiazolyll formamide or N methyl-N-nitrosourea.
A; Reference number: A61204; MUID:92035293; PMID:1682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999.
C;Accession: A44562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A44562; MUID:86118662; PMID:3945311
                                                                                                                                                                                                                                                                                                                                                                                                                       IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDMGGDLVDA
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                                                                          781 YVSKLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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                                                                                                                                       RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDBAYVMAGVGSP
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A;Molecule type: DNA
A;Residues: 637-663.'V',665-702 <MAS>
A;Note: authors translated the codon GCA for residue 25
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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Goment: Amplification and overexpression of this erbB-related gene occurs in about 3C
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A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
C;Function:
C;Function:
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Function:
C;Superfamily: epidermal growth factor receptor; protein; phosphorotein; phosphorotein; phosphorotein; phosphorotein; protein-tyrosine kinase erbB2 #status predicted <ATS-C;Superfamily: epidermal growth factor acceptor; protein: protein-tyrosine kinase erbB2 #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATS-C;Superfamily: extracellular #status predicted <ATMS-C;Superfamily: EGF receptor extracellular domain repeat <AES-C;Superfamily: extracellular #status predicted <ATMS-C;Superfamily: protein kinase homology <ATMS-C;Superfamily: protein kinase homology <ATMS-C;Superfamily: protein kinase Harbus predicted <ATMS-C;Superfamily: protein kinase Harbus predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein kinase predicted <ATMS-C;Superfamily: protein k
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3; Mismatches 12;
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Matches 1240; Conservative
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C.Species: Mesocricetus auratus (golden hamster)
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C.Species: Mesocricetus auratus (golden hamster)
C.Species: Mesocricetus auratus (golden hamster)
C.Succession: 148161
R.Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; I Gene 140, 251-255, 1994
A.;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A.;Reference number: 148161
A.;Reference number: 148161
A.;Reference number: 148161
A.;Accession: 148161
A.;Accession: 148161
A.;Molecule type: mRNA
A.;Residues: 1-1254 <RES>
A.;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
C.;Genetics:
A.;Gene: neu
C.;Superfamily: epidermal growth factor receptor; protein kinase homology
C.;Keywords: ATP
F;718-983/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                           YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLT 1198
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      EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE
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                                                 WMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
                                                                  WMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLLEDDDMGDLV
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86.8%; Pred. No. 2.5e-235;
iive 58; Mismatches 107; I
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Best Local Similarity 86.8<sup>1</sup>
Matches 1089; Conservative
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                                                 (covalent) #status
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                                                                                         predicted
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F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covale: F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                  Mismatches 113; Indels
                                                                                                                      Score 5919; DB 1;
Pred. No. 2.4e-235;
                                                                                                                                                  46;
                                                                                                                      86.9%;
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A; Molecule type: mRNA
A; Residues: 1.1210 <ULL.
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A; Title: Characterization and sequence of the promoter region of the human epidermal grow
A; Reference number: A25772; MUID:85270438; PMID:2991899
                                                                                                                                                                                                                        A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Rocagene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification A;Reference number: S30024; MUID:8821733; PMID:3329716
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
S. Baol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature transcript
A;Reference number: A38672; MUID:91107677; PMID:1988448
number: A00641; MUID:84219729; PMID:6328312
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A,Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 234-297, 1984
A,Reference number: A05281; MUID:84172183;
A,Accession: A05281
                                                                                                                                                                              A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <ISH>
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-29 <HA2>
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A, Molecule type: DNA
A, Residues: 1-29 <HAL>
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A; MOLECULE type: MRNA
A; Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
',798-799,'TD', 802-811,'R',813-942 <XUY>
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF recept
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.N
Science 244, 844; 848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplification .
A; Reference number: A43615; MUID:84196372; PMID:6326261
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R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth factor receptor and superco A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Contents: annotation; receptor activity
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A,Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
Diol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal
A;Reference number: A60143; MUID:85182650; PMID:2985580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 713-964 <LIN>
A; Residues: 713-964 <LIN>
A; Experimental Source: epidermoid carcinoma cell line A431
B; Simmental Sope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A; Reference number: A23062; MUID:85046483; PMID:6093780
                                                                                  Roe,
                                                                                  D.P.;
A;Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y; Ishii, S; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.
Nature 309, 806-810, 1984
                                                                                                                                                            A,Title: Human epidermal growth factor receptor cDNA is A,Reference number: A00642; MUID:84245835; PMID:6330563
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Opidermal growth factor receptor precursor - human NiContains: protein-tyrosine kinase (EC 2.7.1.112) erbB NiContains: protein-tyrosine kinase (EC 2.7.1.112) erbB CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: 15-Nov-1984 #sesquence revision 27-Nov-1985 #text change 11-Jun-1999 CiAccession: A00641; A25772; \$30024; A38672; A00642; A43615; A23062; A05281; A60143; A33 FULITICh, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.; Y. P. H. Nature 309, 418-425, 1984 Asimil growth factor receptor CDNA sequence and aberrant expression of A;Title: Human epidermal growth factor receptor CDNA sequence and aberrant expression of

RESULT

| A,Note: the<br>R,Chen, w.S<br>Cell 59, 33<br>A;Title: Fu<br>A,Reference<br>A,Contents:<br>C,Genemics:<br>A,Gene: GDB<br>A,Gene: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>A,Genes: GDB<br>B,Genes: GDB<br>B | A.Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA R; Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Sell 59, 33-43, 1989 A.Title: Functional independence of the epidermal growth factor receptor from a domain rake feerence number: A3331, MUID:90003233; PMID:2790960 A.Contents: annotation; internalization signal C.Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor of Genetics: A.Gene: GDB:EGFR A.Cross-references: GDB:120610; OMIM:131550 A.Kontents: Dominim of EGF to the receptor; protein kinase homology C.Exportain: Signal sequence #status predicted <81G> C.Superfamily: epidermal growth factor receptor; protein kinase homology C.Exportain: Signal sequence #status predicted <81G> F.25-1210/Product: EGF receptor #status predicted <81G> F.25-45/Domain: EGF receptor extracellular domain repeat <eed> F.25-45/Domain: EGF receptor extracellular domain repeat <eed> F.75-00/Domain: EGF receptor extracellular domain repeat <eed> F.75-00/Domain: EGF receptor extracellular domain repeat <eed> F.75-00/Domain: intracellular #status predicted &lt;1NM&gt; F.70-975/Domain: protein kinase homology <kin> F.710-975/Domain: protein kinase homology <kin> F.710-975/Domain: oreted-pit mediated internalization signal F.79-1210/Region: coated-pit mediated internalization signal F.70-1210/Region: inhibitory F.70-1210/Region: coated-pit mediated internalization signal F.70-1210/Feed (ABF) F.70-1210/Feed (A</kin></kin></eed></eed></eed></eed> | Db 603 NNTL-VWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGMVGALLLLLV 659  Qy 665 VVLGVVFGILIKRRQQKIRKYTWRRLLQETELVBPLTPSGAMPNQAQMRILKETELKVK 724   |
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| ery<br>fch   | tch 45.8%; Score 3117; DB 1; Length 1210; (al Similarity 49.2%; Pred. No. 1.3e-120; 622; Conservative 178; Mismatches 359; Indels 106; Gaps 11 LLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 1  | Qy         1024 LVPQQGFFCPDBAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEBAPRSPLAPSEGAGS 1083           Db  |
| 6 6 6 6  | 69 ASLSFLQDIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLGNUEIIIYVQKN 73  69 ASLSFLQDIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128   | QY         1142 QPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQ 1200           Db         1095 Q-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQ 1143           QY         1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAE 1244           Db         1144PTCVNSTFDSPAHWAQKGSHQISLDNPDXQQDFFPKEAKPNGIFKGS-TAE 1193   |
| cy<br>G  | 189 SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP 247  184 LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGP 243   | 1194 NAEYL 119  |
| ठे व ठे व  | 248 KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD 307   | ASJULT 5 ASJUBS epideranal growth factor receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 18-Jun-1999 C;Accession: ASJ183; A43818; S24942; A28941; A58325; I49643 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.; I |
| o a o  | 368 KKIFGSLAFLPESFDGDPASNTAPLOPEGLOVFETLEEITGYLYISAWPDSLPDLSVFQN 427 363 TSISGDLHILPVAFRGDSFTHTPFLDPQELDILKTVKEITGFLLIQAMPENRTDLHAFEN 422 428 LQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFR 487   | Genes Dev. 8, 399-413, 1994  A;Tile: The mouse waved-2 phenotype results from a point mutation in the EGF receptor t, A;Reference number: A53183; MUID:94170986; PMID:8125255  A;Accession: A53183  A;Accession: A53183  A;Residues: 1-1210 < LUB->   |
| 90 A   | ::     :  :   :    :   | A;Cross-references: GB:U03425 R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991 A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding sit A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Accession: A43818  |
| 6 B 6  | 548 QGLPREYUNARHCLPCHPECQPQNGSVICFGPEADQCVACAHYKDPFFCVARCPSGVKFD 607 :   | A;Molecule type: mRNA<br>A;Residues: 1-714 <avi><br/>A;Cross-references: GB:X59698<br/>R;Eisinger, D.P.; Serrero, G.<br/>submitted to the EMBL Data Library, June 1992<br/>A;Reference number: S24942<br/>A;Accession: S24942</avi>   |

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poidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
S;Species (Gallue gallue)
C;Species (Gallue gallue)
C;Accession: A27720; A00643
R;Lax, I; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstr M.) Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mou A;Reference number: A27720; MUID:88261272; PMID:3260329
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A, Molecule type: mRNA
A, Keaidues 169-971. Xf., 573-1115, To CEIS>
A, Cross-references: BrBU: 212608
A, Cross-references: BrBU: 212608
A, Title: Bpidermal growth factor receptor threonine and serine residues phosphorylated in A. Fielserence number: A28341; MID: 88310814; PMID: 3138233
A, Accession: A2894; MID: 88310814; PMID: 3138233
A, Accession: A2894
A, Description: A2894; MID: 88310814; PMID: 3138233
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: Dum, A. R.; Alexander, W. S.
B, Milbe, M. L.; Dum, A. R.; Alexander, W. S.
A, Accession: S4325
A, Accession: S4325
A, Accession: S4325
A, Accession: S4325
A, Molecule type: DNA
A, Status: Pretainlary
A, Molecule type: DNA
A, Status: Pretainlary
A, Molecule type: DNA
A, Status: Accession of the epidemal growth factor receptor gene is regulated in mouse b, A; Title: Expression of the epidemal growth factor receptor; MID: 68348
A, Accession: 14943; MID: 9112380; PMID: 68348
A, Accession: 14944; MID: 9112380; PMID: 68348
A, Accession: 14944; MID: 911261800; PMID: 683029.1; PID: 9690000
C, Conetactor canador: Actor receptor; Kinase-related transforming protein; phosphopror c, Superfacences: G3: Londer, MID: 91261800; PMID: 68304
A, Accession: 14944; MID: 9191261800; PMID: 68304
A, Accession: 14944; MID: 9191261800; PMID: 68304
A, Accession: 14944; MID: 9191261800; PMID: 68304
C, Superfamily: epidermal growth factor receptor; protein kinase homology
C, Revocade: ATP; growth factor receptor; Kinase-related transforming protein; phosphate (SAP) (Covalent) #status experimental
F, 599, 1070, 10718 Binding site: phosphate (SAP) (covalent) #status experimental
F, 599, 1070, 10718 Binding site: phosphate (SAP) (covalent) #status experimental
F, 1098/Binding site: (or 1997) phosphate (SAP) (covalent) #status experimental
F, 1098/Binding site: phosphate (Thy) (covalent) #status experimental
F, 1098/Binding site: phosphate (Thy) (covalent) #status experimental
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       epidermal growth factor receptor, HER4 - human
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
                                                                                                                                                                                              LEERRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGADEKEYHAEGGKVPIKWMALESIL
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                                                                            VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS
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A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-1308 ePLO>
A; Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology < KIN>
F;724-732/Region: protein kinase ATP-binding motif
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
pecific protein kinase
F;1-10.Domain: signal sequence #status predicted <SIG>
F;31-1223/Product: epidermal growth factor receptor #status predicted <SIT>
F;31-524/Domain: EGF receptor extracellular domain repeat <EE2>
F;31-654/Domain: EGF receptor extracellular domain repeat <EE2>
F;53-677/Domain: EGF receptor extracellular domain repeat <EE2>
F;65-6377/Domain: intracellular #status predicted <TWM>
F;65-6377/Domain: intracellular #status predicted <TWM>
F;71-1984/Domain: intracellular #status predicted <TWM>
F;71-735/Region: protein kinase homology <KIN>
F;72-735/Region: protein kinase ATP-binding motif
F;119-560/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (TMr) (covalent) (by protein kinase C) #status predicted
F;687/Binding site: Lys #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
A;Accession: A27720
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1223 <LAX>
A;Cross-references: GB:M20386
B;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
Cell 41, 719-726, 1985
A;Title: C-exbB activation in ALV-induced erythroblastosis: novel RNA processing and pro
A;Reference number: A00643; MUID:8522822; PMID:2988784
A;Molecule type: mRNA
A;Mesidues: 585-1223 <NIL>
A;Cross-references: GB:M10066
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDLYAFENLEIIRGRIKQHGQYSLAVVNLKIQSLGLRSLKEISDGDIAIMKNKNLCYADT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIYLPINASLSFLQDIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDNGD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 CVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYKDPPFC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGAAVLVLLLGVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPWDQLFRNPHQALLHTANR PEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 45.3%; Score 3085.5; DB 1; Length 1223; al Similarity 48.1%; Pred. No. 2.5e-119; 624; Conservative 177; Mismatches 351; Indels 145;
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|--|----|--|---|-----------|-----|--|---|--|-----|-----|----|-------------|---|---|--|-----|-----|--|----------|--|---|---|-----|------------------|--|--|--|--|---|------|---|
| ery Match 43.3%; Score 2950.5; DB 2; Length 1308; St Local Similarity 45.0%; Pred. No. 8.9e-114; tches 606; Conservative 183; Mismatches 384; Indels 173; Gaps | >  | 9 WVWVSLLVAAĞTVQPSDSQSVCAĞTENKLSSLSDLEQQYRALKKYYENCEVVMĞNLEİTS | 65 LPTNASLSFLQDIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDNGDPLN : | S NTTPVTG |     | S DINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG | SINGSSGCGRCRRSCIG-RCMGFIENRCQIEIRICGASGCGGRCIGFIVSSCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 244 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCYTACPYNY |     | . 🗷 | -E | OSWPPNMTDFS | 24 VFONLOVIRGRILHNGAYSLTLOGLGISWLGIRSLRELGSGLALIHHNTHLCFVHTVPWD | IO VESNEVIIGGEVEISGESEELEINGGGEISSEGEGSGENIIIINNI.<br>OA OI BBNDEGANIIHMAND DBDBGWGBGIAGHOI GABGEMGBGBGGGGMGGGGTBGGRURE | # UNIVERSITING REPORT OF THE PROPERTY OF THE P | ĽΩ  |     | PIWKFPDEEGACQPCFINCTHSCVDLDDKGCPAEQRASPL | 2HAR-TPL | 52 TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQBTBLVBP | IAAGVIGGEFILVIVGEIFAVIVKKKSIK-KKKALKKFE-EIELVEFUIFSGIAKNQ | 711 OMKILKETELKKVKVLGSGARGITYKGIMIPUGENVILVAAKVLKENISPKANKELLUE<br> | ٠ - | :   :   :      : | 831 KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA | 829 KGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKMMA | 891 LESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID | 889 LECIHYRKFTHOSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTID | . 951 VYMIMVKCWMIDSECRPRERLYSEFSRMARDPORFVVIQNED-LGPASPLDSTFYRSLL |      | 1010*EDDDMGDLVDAEEYLVPOOGFFCPDPAPGAGGMVHHRRRSSSTRSGGGDLTLGLEPSEEE |
| Query<br>Best 1<br>Match   | ઠે | qq   | 상<br>음  | à         | QQ  | ठे व   | 9   | දු දු  | ò   | qq  | ò  | <b>q</b> a  | \$ 8  | 8 8   | S 8  | ò   | 셤   | ò  | g        | हे ह   | Ω (   | è   | 3 8 | ; a              | ò  | qq   | ò  | g  | È   | QQ   | è   |

protein-tyrosine kinase (BC 2.7.1.112) mrk-Y precursor - southern platyfish NyAlternate names: epidermal growth factor receptor homolog, kinase-related transforming C;Species: Xiphophorus maculatus (southern platyfish) (c;Species: Xiphophorus maculatus (southern platyfish) (c;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000 (c;Accession: S06142; S13809 (c;Accession: S06142; S13809 (c;Accession: Mature 31, 415-421, 1989) Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, A.; Roberts Nature 31, 415-421, 1989 (c;Accession: S06142; MuID:90015140; PMID:2797166 A,Molecule type: DNA
MyResidues: 1-1166 < WIT>
MyResidues: 1-1166 < WIT>
A;Cross-references: EMBL.X16991; NID:g65290; PIDN:CAA34770.1; PID:g65291

R;Adam, D.; Maeueler, W.; Schartl, M.
Rocogene 6, 73-80, 1991
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophoru A;Reference number: S13807; MUID:91125882; PMID:1846957 A, Map position: Y
A, Introns: 872/3; 888/1; 947/1; 979/3; 1025/3; 1056/1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; tyro
F;1-25/Domain: signal sequence #status predicted <5IG>
F;1-25/Domain: protein kinase transforming protein (Tu) #status predicted <MAT>
F;707-972/Domain: protein kinase Anp-binding motif 1212 1101 LPTHDPSPLORYSEDPTVPLPS-----ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR 1153 -----FSPAFDNLYYWDQDPPERGA--PPSTF 1237 1200 DEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKAFDNPDÝWNHSLPPRSTLQHPDYL 1259 119 28 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 29 62 60 LELTYLPTNASLSFLQDIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDN 8 AALLQ--LLLVLSISRCCSTDPDFKVCQGTSNQMTM---LDNHYLKMKKMYSGCNVVLEN 4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN -- PLAP-SEGAGSDVFDGDLGMGAAKGLQS EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA-Gaps A,Molecule type: DNA A,Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA> A,Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285 Indels 138; Length 1166; Query Match
39.0%; Score 2653; DB 1;
Best Local Similarity 44.8%; Pred. No. 1.2e-101;
Matches 568; Conservative 163; Mismatches 398; ----- 1249 QEYSTKYFYKONGRIRPIVAENPEYL 1285 A; Status: preliminary; translation not shown KGTPT---------1070 APRS---A; Accession: S13809 A; Accession: S06142 1260 1009 1154 1168 1213 1238 63 120 셤 ò a ö ò &. 명 ò g 셤 ò 셤 ò 셤 ∂

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| VSHNPLLCNVETINWWDIVDKTSNP 179        | LIRIVCAGGC-ARCKGPLPIDCCHE 238                                  | FTKLLCAEQČNRŘCRGPKPIDČČNE 239         | YNIDTFESMPNPEGRYTFGASCVTA 298<br> : : :     :             :  <br>YDIVSHQVVDNPNIKYTFGAACVKE 299 | 35   | 4 4   |   | OLCARGHCWGPGPTQCVNCSQFLRG 537<br> :                  <br>NECSEDGCW-PGPTMCVSCLHVDRG 529 | SVICEGPEADQCVACAHYKDPPFCV 597<br> :  :                         | SCVDLDDKGCPAEQRASPLTSIVSA 657<br>                 <br>3CSGPGLSGCRGD-IVSHSSLAVGL 647 | ETELVEPLTPSGAMPNQAQMRILKE 117<br> | KVLRENTSPKANKEILDEAYVMAGV 777<br>             : :                | NRGRLGSQDLLNWCMQIAKGMSYLE 837<br>::                       <br>4QERICGQWLLNWCVQIAKGMNYLE 826 | DETEYHADGGKVPIKWMALESILRR 897<br>                              | OLLEKGERLPOPPICTIDVYMIMVK 957<br>                                | DIGPASPLDSTFYRSLLEDDDMGDL                                    | RSGGDLTLGLEPSEEAPRSPLAP 1077<br> | SEDPTV-PLPSETDGYVAPLTCSPQ 1136<br>                         | KNGVVKD 118 | SSQEAETNFSRPEYLNTNQNSL 1111 | PPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTA 1243<br>                      |
|--------------------------------------|--|---------------------------------------|--|--|-------|---|--|--|---|-----------------------------------|--|---|--|--|--|----------------------------------|--|-------------|-----------------------------|--|
| 3 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKV | 0 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE | O TMNLIPHAFERQCQKCDHGCVNGSCWAPGPGHCQK | 9 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA                                 | 9 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS |       | 9 LPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFV :             :       :    : |  | 9 QECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV | ARCPSGVKPDLSYMPIWKFPDEBGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA                        |                                   | TELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGV<br> | GSPYUSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLE<br>                            | DVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRR:: | RFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVK<br> | CWMIDSECRPRERELVSEFSRMARDPQREVVIQNEDLGPASPLOSTFYRSLLEDDDMGDL |                                  | SEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVA <br> |             | •                           | VFAFGGAVENPEYLTPQGGAAPQPHP<br> :::: :       <br>PLVSSGSMDDPDYQAG |
| . 123                                | 8  | 180                                   | 239  | 299  | 359   | 419   | 478  | 538<br>530   | 898<br>065  | 658<br>648                        | 718  | 778   | 838<br>827   | 898<br>887   | 958<br>947   | 1018                             | 1078   | 13          | 1056                        | 1184   |
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C;Species: Homo sapiens (mān)
C;Species: Homo sapiens (mān)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
C;Accession: A36223; I59164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
A;Title: Solation and characterization of ERBB3, a third member of the ERBB/epidermal g;A;Reference number: A36223; MUID:90083234; PMID:2687875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Residues: 1-1342 <KRA>
A;Cross-references: GB:M29366
B;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-re A;Reference number: I59164; MUID:90311312; PMID:2164210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GDB:119880; OMIM:190151
A;Map position: 12q13-12q13
(S.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homolo C;Keywords: ATP; phosphotransferase F;707-972/Pomain: protein kinase homology <KIN> F;715-723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NASLSFLQDICEVQOYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAG 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.1%; Score 2389.5; DB 2; Length 1342; Best Local Similarity 40.2%; Pred. No. 8.5e-91; Matches 527; Conservative 189; Mismatches 466; Indels 129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: IS9164
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 <RES>
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
C;Genetics:
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                                                 1150 ENLEYLG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: ERBB3; HER3
ENPEYLG
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A36223
1244
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Thr and GTT for residue : transduces signals to the

Annue: Ine authors translated the codon AAC for residue 369 as 'C,Comment: This protein is a functional heregulin receptor that (C,Genetics:

A, Experimental source: liver A, Note: The authors translated the

GB:U29339; NID:g915389; PID:g915390

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A; Gener: ExbB3
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C; Superfamily: growth factor receptor; liver; phosphoprotein; transmembrane protein F; 1-139/Domain: signal sequence #status predicted <SIG»
F; 20-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F; 640-659/Domain: transmembrane #status predicted <TMM>
F; 705-97/Domain: protein kinase homology <KIN>
F; 713-721/Region: protein kinase ATP-binding motif
F; 713-721/Region: protein kinase ATP-binding motif
F; 939, 1051, 1156, 1194, 1196, 1219, 1257, 1259, 1273, 1286, 1325/Binding site: phosphate (Tyr) (cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSSGY-MPMNQGNLGESCQESAVSGSSERCPRPVSLH-----PMPRGCLASESSEGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 TGSEAELQEKVSMCRSRSRSRSPPPRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVM
                                     FRNPHQALLHTA-NRPEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECYEEC
                                                             RVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGV
                                                                                                                                          KPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSAVVG
                                                                                                                                                                                                                      ILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE
                                                                                                                                                                                                                                                                                                                   --LVVIFMMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPS-EKANKVLARIFKETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APSEGAGSDVFDGDLGMGAAKGLQSLPTHD-PSPLQRYSEDPTVPLP----SETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEYLTPQGGAAPQPHPP
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NLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDPPERGAPPSTFKGTPTAENPEYL 1249
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JC4387
epidermal growth factor receptor homolog precursor - rat
epidermal growth factor receptor homolog precursor - rat
epidermal growth factor receptor homolog precursor - rat
N,Alternate names: ErbB3 procein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Accession: JC4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the re
A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Accession: JC4387
A;Molecule type: mRNA
A;Residues: 1-4339 <HEL>
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                                                                                                                                         ---LNYNT----NSSHALRQLKFTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR---
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                                                                                                   QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
                                                                                                                                                                                                                                                            CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS
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                                                                                                                                                                                                                                                                                                       ANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEOLOVFETLEEITGYLYISAWPDS
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                                                                                                                              GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL
                                                                                                                                                                         ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMR
                                            LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
Ouery Match 34.0%; Score 2316.5; DB 2; Length 1339; Best Local Similarity 40.4%; Pred. No. 8.3e-88; Matches 518; Conservative 170; Mismatches 440; Indels 155;
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| Db 117 GLECCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172 Qy 697 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756 | 757 ENTSPRANKEILDEAYWAGVGSPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGR<br>     | Oy 817 LGSQDLIAWCMQJAKGMSYLEDVRLUHRDLAARNYLVKSPHYKTTDFGLARLLDIDETE 876<br> | Qy 877 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 936    : | Qy 937 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 995 | QY 996 PASPLDSTFYTSLLEDDDWGDLVDAEKYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSG 1055 | QY 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110 | QY 1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEXVNQPDVRPQPPSPREGPLPAARPAGATLE 1168 | Qy       1169 RAKTLSPGKNGVVKDVFAFGGAVENDEYLTPQGGAAPQPHPPAF 1213         b       :   : | RESULT 12  TVYUH  protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)  C;Species: avian erythroblastosis virus  C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999  C;Accession: A00644, A38022 | R; Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. Cell 35, 71-78, 1983 A; Title: The erbB gene of avian erythroblastosis virus is a member of the src gene famil) A; Reference number: A00644; MUID:84026539; PMID:6313229 | A; Accession: Avoint<br>A; Residues: 1-604 < YAM><br>A; Residues: 1-604 < YAM><br>A; Cross-references: GB: K01216; NID: 9209676; PIDN: AAA42400.1; PID: 9209678<br>R; Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin,<br>Science 224, 1456-1459; 1984<br>A; Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of<br>A; Reference number: A38022; MUID: 84223957; PMID: 6328658  | A; Molecule type: DNA A; Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 <deb> A; Cross-references: GB: K02006 A; Cross-references: GB: K02006 C; Genetics: A; Gene end: A; Gene end: C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p) F; 130-135 (Domain: protein kinase homology <kin> F; 130-135 (Domain: protein kinase ATP-binding motif F; 165/Active site: Lys #status predicted</kin></deb> |
|--|---|--|--|---|--|--|---|---|--|--|--|---|
| 761<br>834<br>821  | 894 ILERRETHGSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLEQPPICTIDVYM     :: | OY 554 IMVACUMILDSECREFREIVSEFSRMARDPORFVVIONEDIGFARSLIEDDD 1013 :         | QY 1014 MGDLVDABEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE 1068  1      | QY 1069BAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD 1105<br>                   | OY 1106 PSPLORYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 1145                    | Qy 1146 RPQPPSRRGPLPAARPAGATLERAKTLSP-GKNGVVKDVFAF 1187              | Oy 1188 GGAVENDEYLTPOGGAAPOPHPP 1210  Db 1192EEYEXMNRKRGSP-PRPP 1209    | nase<br>Raines, N   | ig and pro   | .1750<br>Ballus gal  | C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;1-6/Product: gag protein (fragment) #status predicted <gmo> F;7-59/Product: env protein (fragment) #status predicted <gmo> F;0-698/Product: protein-tyrosine kinase erbB #status predicted <erb> F;0-698/Product: protein-tyrosine kinase erbB #status predicted <erb> F;202-210/Region: protein kinase ATP-binding motif F;229/Active site: Lys #status predicted</erb></erb></gmo></gmo> |   |

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A/Gene: FlyBase:Egfr
A/Cross-references: FlyBase:FBgn0003731
A/Gene: FlyBase:Egfr
A/Cross-references: FlyBase:FBgn0003731
ClyBayords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphoprotein: extracellular #status predicted <EXT>
F/1-732/Domain: extracellular #status predicted <EXT>
F/133-764/Domain: intracellular #status predicted <IVM>F/33-764/Domain: intracellular #status predicted <IVM>F/33-764/Domain: protein kinase homology <EXIN>F/808-1072/Domain: protein kinase homology <EXIN>F/808-1072/Domain: protein kinase ATP-binding moif
F/816-824/Region: protein kinase ATP-binding moif
F/816-824/Region: protein kinase ATP-binding moif
F/816-824/Region: protein kinase ATP-binding moif
F/8174/Binding site: phosphate (TYR) (covalent) (by protein kinase C) #status predicted
F/8181/Binding site: Lys #status predicted
F/8181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
A;Wolecule type: DNA
A;Residues: 'A', 832-866,'V',868-943,'QTPSLVK' <WAD>
A;Cross-references: EMBL:X02293; NID:97922; PIDN:CAA26157.1; PID:9929565
C;Comment: This sequence is tentative because the introns have not been identified.
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N; Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

N; Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C; Species: Drosophila melanogaster
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change.11-Jun-1999

C; Accession: A00640; A38021

R; Livueh, B.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.

Cell 40, 599-607, 1985

A; Title: The Drosophila EGF receptor gene homolog: conservation of both hormone binding
A; Reference number: A00640; MUD:85124611; PMID:2982499

A; Accession: A00640

A; Molecule type: DNA
A; Residues: 1-1330 elliv
A; Cross-references: EMBL:K03054

R; Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature 314, 178-180, 1985
A; Title: A Drosophila genomic sequence with homology to human epidermal growth factor re
A; Reference number: A38021; MUID:85137938; PMID:2983232
A; Accession: A38021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 ICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHLPSPTDSKF 417
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                                                                                                                                                                                                                                                                              118 APNQAHLRILKETEFKKVKVLGSGAFGTIYKGLWIPEGEKVKIPVAIKELREATSPKANK 177
                                                                                                                                                                                                                                                                                                                                            EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW 825
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                                                                                                                             CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP--- 58
                                                                                                                                                                                                                                                                                                                                                                  ----NTNQSPLAKTVFE
                                                                                                                                                                       RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                              Gaps
25.0%; Score 1703; DB 1; Length 604;
52.2%; Pred. No. 5e-63;
ive 76; Mismatches 128; Indels 126;
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Query Match
Best Local Similarity 52.2
Matches 360, Conservative
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Page 13

| 00   038   DDKGCPAEGRASPL/SIVSANV-GILL/WVLGVPGILIKRROCKIRKYTARRLIOFTEL 696   58   GLEGCPRGSKTPSIAAGVVGGLCLWVVGGGGLALRRR-HIVRKRTLRRLIOFTEL 113   114   1    | Subjectives avian erythroblastosis virus C;Decies: avian erythroblastosis virus C;Decies: avian erythroblastosis virus C;Decies: avian erythroblastosis virus C;Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C;Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C;Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C;Date: 020072 R;Scotting, P:;Vennstron, B:;Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J. R;Accession: S00727;MulD:88217326;PMID:2897102 A;Accession: S00727;MulD:88217326;PMID:2897102 A;Molecule type: DNA A;Molec |
|--|--|
| 0.000   0.00 | PRESULT 14  S15745  protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;ppecies: avian erythroblastosis virus C;ppecies: avian erythroblastosis virus C;pate: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S15745 R;Vennstroen. B. A;Reference number: S15745 A;Aolecule type: DNA A;Residues: 1.544 «VEN> A;Reference number: S15745 A;Aolecule type: DNA A;Residues: 1.544 «VEN> A;Cross-references: EMBL:X12707 C;Genetics: A;Genetics: A;Gene: erbB C;Genetics: A;Genetics: 
|        | LPMDSRYQNSHSTAV  | 524  | QC         |
|--------|--|------|------------|
|        | AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197                            | 1170 | ò          |
| K 523  |  | 482  | ф          |
| R 1169 | RYSEDPTVPLPSETDGYVAPLICSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER | 1111 | ò          |
| - 481  | SRIPLLSSLSATSNNSATNCIDRNGG                                   | 455  | d<br>D     |
| 2 1110 | GGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ      | 1056 | ò          |
| - 454  | LPSPTDSKFYRTLMEEEDMEDIV                                      | 414  | g          |
| 3 1055 | PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAFGAGGMVHHRHRSSSTRSG | 966  | ò          |
| Н 413  | KGERLPQPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMH | 354  | qq         |
| 3 995  | KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQF            | 937  | ò          |
| g 353  | YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE | 294  | q          |
| E 936  | YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE | 877  | ò          |
| E 293  | IGSQYLLNWCVQIAKGM  | 234  | qq         |
| E 876  | LGSQDLLNWCMQIAKGMSYLE  | 817  | ò          |
| N 233  | EATSPKANKBILDEAYVWASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIRBHKDN | 174  | . <b>Q</b> |
| R 816  | ENTSPKANKEILDEAVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLD          | 757  | ò          |
| R 173  | VEPLTPSGEAPNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELR | 114  | q          |
| R 756  | VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKG                    | 697  | ò          |

Search completed: July 22, 2003, 09:08:02 Job time : 31.9062 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec

Perfect score: Sequence:

SEQ4-103-117-12
6809
1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB B Maximum DB B

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
2: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f | protein-tyrosine k | protein-tyrosine k | epidermal growth f | protein-tyrosine k | kinase-related tra | protein-tyrosine k | protein-tyrosine k | ¥      | protein let-23 (im | protein-tyrosine k | yrosine | growth |        |        | protein-tyrosine k | protein-tyrosine k | insulin-like growt | insulin receptor p | insulin receptor p |
|-----------|---------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|---------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID            | A24571             | TVRTNU             | 148161            | GOHUE              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV             | TVYUH              | GQFFE              | S35745             | S00727             | B44776             | TVFVEB             | A36325 | E88257             | 870712             | 870713  | A45558 | A42032 | A27131 | S13807             | S13808             | T43220             | INHUR              | A36080             |
|           | 80            | н                  | -                  | ~                 | -                  | ~      | ٦      | 7      |        | ď                  | N                  | -                  | Н                  | Н                  | 7                  | ~                  | 7                  | ٦                  | 7      |                    |                    |         |        | 7      | 7      | 7                  | 7                  | ~                  | Н                  | 7                  |
|           | Length        | 1255               | 1260               | 1254              | 1210               | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698                | 604                | 1330               | 544                | 545                | 540                | 540                | 644    | 1323               | 1374               | 1369    | 1717   | 527    | 843    | 346                | 311                | 1363               |                    | 1383               |
| de        | Query         | 98.8               | 87.5               | 87.3              | 46.4               | 46.0   | 45.7   | 4      | 39.6   | 35.6               | 34.3               | 25.9               | 25.0               | 24.3               | 24.2               | 24.1               | m<br>m             | 23.8               | 22.3   | 19.3               | 19.3               | 18.0    |        | •      |        | 11.8               | 11.1               | 10.8               | 10.6               | 10.5               |
|           | Score         | 6730               | 5957               | 5941.5            | 3160               | 3130   | 3113.5 | 3003.5 | 2699   | 2421.5             | 2336.5             | 1766.5             | 1703               | 1654.5             | 1647               | 1640               | 1623               | 1621               | 22     | 1311               | 3                  | 22      | 16     | ◡      | 999.5  |                    | 754.5              | 733                | 720                | 713                |
|           | Result<br>No. | н                  | 8                  | m                 | 4                  | Ŋ      | 9      | 7      | 80     | φ.                 | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 |                    | 17                 | 18     | 19                 | 20                 | 21      | 22     |        | 24     | 25                 | 26                 | 27                 | 28                 | 29                 |

| insulin receptor p | insulin-like growt | insulin receptor-r | protein-tyrosine k | insulin receptor-r | insulin-like growt | insulin receptor - | insulin-like growt | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | tyrosine kinase Mp | protein-tyrosine k | mouse developmenta | protein-tyrosine k |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A34157             | T43212             | A36502             | T18534             | B36502             | IGHUR1             | T30346             | A33837             | A56081             | S57245             | A54092             | 150612             | S49004             | S05582             | 148652             | 833596             |
| N                  | ~                  | N                  | N                  | 7                  | н                  | (7                 | ~                  | ч                  | N                  | N                  | 7                  | ~                  | Н                  | 7                  | 7                  |
| 1372               | 1607               | 1300               | 1477               | 1268               | 1367               | 1390               | 1371               | 2148               | 2101               | 987                | 952                | 977                | 1114               | 987                | 1001               |
| 10.5               | 10.2               | 10.1               | 10.0               | 6.6                | 9.6                | 9.5                | 9.4                | 9.1                | 9.1                | 8.9                | 8.7                | 8.7                | 9.8                | 9.8                | 8.6                |
| 712.5              | 694                | 684.5              | 684                | 672                | 651                | 644                | 640                | 622.5              | 617                | 605                | 591.5              | 589.5              | 588                | 587                | 586                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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| 3 | 571 |
| 2 | S   |

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erb C;Species: Homo sapiens (man) (5,Species: Homo sapiens (man) (5,Species: Homo sapiens (man) (5,Species: 15-0ct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999 (5,Accession: A24571; A25491; A44188; B44188; IS9509; I57622 (5,Accession: A24571; A25491; A44188; B44188; IS9509; IS7622 (A7amanoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Nature 319, 230-234, 1986 protein encoded by the human c-erb-B-2 gene to epidermal growth A;Reference number: A24571; MUID:86118663; PMID:3003577

A;Accession: A24571

A;Molecule type: mRNA A;Residues: 1-1255 cYAN-A;Residues: 1-1255 cYAN-A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. R;Semba, K.; Kamata, N.; Toyoshima, E.; Yamamoto, T. A;Title: A v-erbB-related protoconcogene, c-erbB-2, is distinct from the c-erbB-1/epider-A;Reference number: A25491; MUID:86016729; PMID:2995967

Seeburg, ٦. A;Accession: A25491
A;Molecule type: DNA
A;Residues: 737-1031 <SEM>
A;Fesidues: 737-1031 <SEM>
A;Cross-references: GB-11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Cross-references: GB-11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
Cross-references: GB-11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
B;Cross-references: GB-1139; NID:g185

A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromo A;Reference number: A44188; MUID:86070181; PMID:2999974

A; Accession: A44188

A;Molecule type: DNA A;Residues: 740-910 <COUI> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A,Molecule type: mRNA A,Rosidues: 1-517, RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2> A,Cross-references: GB:M11730, NID:9183966 R;King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1988 A,Fitle: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A,Reference number: 159509; MUID:85272597; PMID:2992089

A; Accession: I59509

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 832-909 < REX>
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu) Promoter: evidence for multiple mechanisms for transcriptiona
A;Reference number: IS7622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL>

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Processin-tyrosine kinase (BC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Decies: 31-Dec-1988 #text_change 11-Jun-1999
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Accession: A24562
A;Accession: A24562
A;Accession: A24562
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1.1260 *ABR>
A;Residues: 1.1260 *ABR>
A;Residues: 1.2560 *ABR>
A;Residues: 1.2560 *ABR>
A;Residues: 1.2560 *ABR>
A;Residues: MUD: B6118662; PMID: 3945311
A;Rile: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no 2-thiazoly] formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204
A;Status: preliminary
A;Accession: A61204
A;Residues: 637-663, VV, 665-702 *AMAS>
A;Residues: 637-663, VV, 665-702 *AMAS>
A;Residues: 637-663, VV, 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
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A;Residues: 637-663, VV; 665-702 *AMAS>
A;Residues: 637-663, VV; 665-702 *AMAS>
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A;Residues: 637-664 *AMAS>
A;Residues: 637-664 *AMAS>
A;Residues: 637-665 *AM
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                                                  ILLVVVLGVVEGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                        RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
                                                                                                                                                                   YVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                                                                                                                                                                                                                 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                                                                   A/Gene: GDB.ERBB2; NGL; NEU; HER-2
A/Cross-references: GDB.120613; OMIM.164870
A/Cross-references: GDB.120613; OMIM.164870
A/Cross-references: GDB.120613; OMIM.164870
A/Introns: 155/1; 75/3; 147/1; 893/3
A/Note: the list of introns is incomplete
C/Function:
A/Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C/Superiamily: epidermal growth factor receptor; protein kinase homology
C/Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
                                                                                                                                                                                                                                                                                                     Fig. 121/Domain: signal sequence #status predicted <SIG>
Fig. 21/Domain: signal sequence #status predicted <SIG>
Fig. 21/S5/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
Fig. 25/Domain: extracellular #status predicted <EE1>
Fig. 25/Domain: EGF receptor extracellular domain repeat <EE2>
Fig. 25/Domain: EGF receptor extracellular domain repeat <EE2>
Fig. 25/Domain: irransmembrane #status predicted <TMM>,
Fig. 25/Domain: irransmembrane #status predicted <TMT>
Fig. 25/Domain: protein kinase homology <KIN>
Fig. 124/Region: protein kinase ATP-binding motif
Fig. 21/B7/25/Sig. 530, 571, 629/Binding site: carbohydrate (Asn) (covalent) #status predicted
Fig. 86/Finding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
Fig. 753/Active site: Lys #status predicted
Fig. 753/Active site: Lys #status predicted
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    PIDN:AAA58637.1; PID:g553332
of this erbB-related gene occurs
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A;Cross-references: GB:M16792; NID:g183983;
C;Comment: Amplification and overexpression
C;Genetics:
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Best Local Similarity 98.9
Matches 1241; Conservative
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Yamazaki, Y.; Ishikawa
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                                                   WMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
                                                                 DAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPS
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87.1%; Pred. No. 1.3e-236;
live 58; Mismatches 103;
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Best Local Similarity 87.1
Matches 1093; Conservative
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                                                                                                                                                                                                                  63
F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;721-739/Region: protein kinase ATP-binding motif
F;711-191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
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                                                                                                                         Score 5957; DB 1;
Pred. No. 3.1e-237;
51; Mismatches 106;
                                                                                                                          87.5%;
                                                                                                                         Query Match
Best Local Similarity 87.49
Matches 1098; Conservative
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A, Reference: Ball.: N. Y. Stratton, R. H.; Roe, B. A.; Marlino, G.T.; Pastan, I.
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A, Reference number: A25772; MUID: 85270418; PMID: 2991899
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A, Reference number: A25772; MUID: 8110313; PMID: 2991899
A, Reference number: S30024; MUID: 88217333; PMID: 3329716
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Nature 309, 418-425, 1984
A,Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of
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| 129 KANSKFIGITELQLRSLTEILKGGVLJQRNPQLCYODTILWKDIFHKNNQLALTLIDTNR 188  127 -ANKTGLKELPMRNLQEILHGAUFENNPALCNUSZIGWEDLYSSDFLSNMSMDFONH 183  189 SRACHPCSPMCKGSRCWGBSEDCOSLTRYLVCAGGCA-RCKGPLPTDCCHGCAAGCTGP 247  184 LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQCSGRCRGKSPSDCCHNQCAAGCTGP 243  248 KHSDCLACLHFWHSGICELHCPALVTYNTDTFESMRNPEGRYFFGASCVTACPYNYLSTD 307  244 RESDCLVCRKFDEATCKDTCPPLMLYNPTTYQMDVNPEGRYFFGACVKCPRNYVYDD 303  308 VGSCTLVCPLHNOEVTAEDCTGCRCKCKGCPCRVCVGIGIGEFKDSLSINATNIKHFRAC 362  364 HGSCVRACGADSYEM-EEDGVRKCKKCEGPCRVCVGIGIGEFKDSLSINATNIKHFRAC 362  368 KKIFGSLAFLBESFDGDPASNTAPLQPEOLQVFTLEEITGYLYISAWPDSLPDLSVPON 427   | 1245 NPEYL 1249  1144PTCVNSTPDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKFNGIFKGS-TAE  11245 NPEYL 1249  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1194 NAEYL 1198  1195 # Extraction O6-Jan-1995 # text change 18-Jun-1999  125pecies Mus musculus (house mouse)  126-Signed Signed φ

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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
R;Lax, I.; Johnson, A.; Howk; R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennst Mol. Cell. Biol. 9, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mo A;Reference number: A27720; MUID:88261272; PMID:3260329
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                424 VFONLOVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
                                                                                                QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE
                                                                                                                                  CRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG
                                                                                                                                                                                                                                 CNILEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAG
                                                                                                                                                                                                                                                                                 604 VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILL
                                                                                                                                                                                                                                                                                                        664 VVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRK
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A.Residues: 659-971, K., 973-1115, D. KEIS.
A.Residues: 659-971, K., 973-1115, D. KEIS.
A.Residues: 659-971, K., 973-1115, D. KEIS.
A.Residues: 659-971, K., 973-1115, D. M.
J. Biol. Chem. 263, 13122-13182, 1988
A.Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in A.Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in A.Releance number: A28941; MUID: 88330814; PMID: 313823
A.Accession: A2894; X., 658-69-704, L., 706-707,989-992, XX', 995-996, X', 998-1000;1002-1009, R.Hibbs M.L.; Dunn, A.R.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, W.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.; Alexander, M.S.;
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46.0%; Score 3130; DB 2; Length 1210;
Best Local Similarity 49.5%; Pred. No. 2.5e-121;
Matches 630; Conservative 171; Mismatches 361; Indels 110;
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epidermal growth factor receptor, HER4 - human
C;Species: 18mc sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
A;Title: Ligand-specific activation of HER4/p180erbB4, a fourth member of the epidermal
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    ||::| :|| || || || CVKQCNILCGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHFIDGPHC
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                                                                    VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS
                                                                                                     VKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---NGSKTPSIAA
                                                                                                                                                         657 AVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL
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| 24.3<br>23.7<br>30.3<br>29.7<br>36.3<br>35.5 | 415<br>415<br>483<br>475<br>543                                  | 602 N. Adam, D.; Medueler, W.; Schall, M.; 602 N. Title: Transcriptional activation of the A; Reference number: \$13807; MUID:9112588 A; Accession: \$13809 A; Status: preliminary; translation not shown as the A; Residues: \$21-1025, N.; 1027-1098, A.; 105 C; Genetics: 710 C; Genetics: A; Map position: Y 708 A; Map position: Y 708 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y 709 A; Map position: Y | 770<br>768<br>830<br>828<br>890<br>888                              | 950  |
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|  | 364 FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDGLPDLS | 544 CRVLQGLPREYVNARHCLPCHPECOP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPS [  | 711 QMRILKETELRKUVULGSGAFGTUYKGIWIPDGENUKIPVAIKULRENTSPKANKEILDE  - | 891 LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 950 |
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mxk-Y precursor - southern platyfish
ctor receptor homolog; kinase-related transformin
hern platyfish)
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                                                        -----PLAP-SEGAGSDVFDGDLGMGAAKGLQS 1100
                                                                                 YRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPVA 1116
                                                                                                                                  ----EIDGYVAPLICSPQPEYVNQPDVRPQPPSPR 1153
                                                                                                                                                          -----FSPAFDNLYYWDQDPPERGA--PPSTF 1237
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ismatches 387; Indels 146; Gaps
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65284; PIDN:CAA39763.1; PID:g65285
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| qa             | 123YQKNPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDK 175   | Ov 1240 TPTABNPEYIG 1250  |
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| & a            | 176 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD 234 :   | 1146 LPAAENLEYLG  |
| රු සි          | 235 CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 294   :      :    :      236 CCNEHCAGCTGPRATDCLACRDFNDGTCKDTCPPRKIYDTVGHOVUNNKYFFGA 295   | RESULT 9 A36223 kinasa-ralated transforming protein (erbp3) (RC 2 7 1 -) precursor - human  |
| े हें          | CUTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR 35  | C;Species: Homo sapiens (man) C: C;Species: Homo sapiens (man) C;Species: Howo sapiens (man) C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 C;Accession: A36223; I59164  |
| 3 & 3          | 296 CYRECEPNIYVE E-GACKRSCBAGMLEVV-ENGARSCRYCLGGVCFKVUGGIGGGSENTI 353 355 AVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEOLOVFETLEEITGYLXISA 414 354 AVNSTNIRSFSKYTKINGDIILARNSFGDPHYKIGTMDPEHANITTVKFTTGYLVIM 413 | KrkTaus, M.H.; Isbaing, W.; MIXL, T.; FUGDBSCU, N.C.; Aaronson, S.A. Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989 A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Acression: A36223         |
| රු පු          | WPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTH 47  | A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1342 <rra> A;Cross-references: GB:M29366</rra>  |
| & 43           | 474 LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ 533   | R;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G<br>Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990<br>A;Title: Molecular cloning and expression of another epidermal growth factor receptor-r<br>A;Reference number: I59164; MUID:90311312; PMID:2164210 |
| 6 64<br>6      | 534 FLRGGECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDP 593   | A;Accession: I59164 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 <res></res>  |
| <i>∂</i> ; 8   | 594 PFCVARCPSGVKPDLSYMPIMKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLIS 653   | A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841<br>C. Genetics: A;Genetics: A;Genesics: A;Genesics: A;Cross-references: GDB:119880; OMIM:190151  |
| 상 원            | 654 IVSAVVGILLVVVLGVVPGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQMR 713<br>   | A;Map position: 12q13-12q13<br>C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol<br>C;Keywords: ATP: phosphotransferase<br>F;707-972/Domain: protein kinase homology <kin></kin>  |
| % <sup>Q</sup> | 714 ILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAXV 773<br>   | F;715-723/Region: protein kinase ATP-binding motif Query Match Best Local Similarity 40.4%; Pred. No. 3.1e-92;  |
| δ q            | 774 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM 833<br>   | Matches 530; Conservative 192; Mismatches 460; Indels 129; Gaps 10 GLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT     :   |
| <i>ò</i> 93    | 834 SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES 893<br>   | 11 GLLFSLARG;SEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH 68 NASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNQY  |
| ъ<br>Вр        | 894 ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM 953   | 71 NADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLN 128 IKANSKFIGITELQLRSLTBILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTN  |
| oy<br>Op       | 954 IMVKCWMIDSECRPRERELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1013  ::  | 123 YNTNSSH-ALRQEKELTQETEILSGGVYIEKNDKLCHMDTIDWRDIVRDRDAEIVVKD 188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG   |
| è d            | 1014 MGDLVDAEEXLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS 1073<br> -  -  -  -  |   |
| ò q            | 1074 PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVAPLT 1132   | 307   |
| ò 8            | 1133 CSPQPEYVNQPDVRPQPPSPREGPLP-AARPAGATLERAKTLSPGKNG 1179   | 367 CKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPFFFFQ   |
| è 8            | 1180 VVKDVFAFGGAVENPEYLTPGGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKG 1239   | ON 427 NLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQL 485   |

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                                                                      604
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Cypecies: Rattus norvegicus (Norway rat)
Cybate: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
CyAccession: JC4387
RyHellyar, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombina
A;Reference number: JC4387; MUD:96096535; PMID:8522190
A;Accession: JC4387
A;Residues: 1-j339 <HEL>
                                                                                                                                    LG--AKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTVIAG
                                                                                                                                                                                 --LVVIFWMLGGTFLYWRGRRIQNKRAMRRYLERGESIEPLDPS-EKANKVLARIFKETE
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                                                                                   PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDV
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NLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANRQLCYHHSLNWTKV
                      FRNPHQALLHTA-NRPEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEEC
                                    LRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGGWGPGPGOCLSCRNYSRGGVCVTHC
                                                                      RVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGV
                                                                                                                     KPDLSYMPIWKPPDEEGACOPCPINCTHSCVDLDDKGCPAEORA----SPLTSIVSAVVG
                                                                                                                                                                     ILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE
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A;Cross-references: GB:U29339; NID:g915390
A;Experimental source: liver
A;Note: The authors translated the codon AdC for residue 369 as Thr and GTT for residue C;Comment: This protein is a functional heregulin receptor that transduces signals to t C;Genetics: This protein is a functional heregulin receptor that transduces signals to t G;Genetics: ErbB3
A;Gene: ErbB3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein F;1-19/Domain: signal sequence #status predicted <SIG-F:10-100main: signal sequence #status predicted <SIG-F:00-1339/Product: epidermal growth factor homolog #status predicted <MMN-F:705-97/Domain: protein kinase homology <KIN-F:705-97/Domain: protein kinase homology <KIN-F:713-721/Region: protein kinase ATP-binding motif F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr)
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34.3%; Score 2336.5; DB 2;
Best Local Similarity 40.5%; Pred. No. 9.4e-89;
Matches 520; Conservative 172; Mismatches 436;
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seq4-103-117-12.rpr

| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172 Qy 697 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756    | QY 757 ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 816 | QY 817 LGSQDLLNW-MQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 876<br> | QY 877 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKBYDGIPAREIPDLLE 936  | QY 937 KGBRLPQPPICTIDVYMINVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 995 | QY 996 PASPLDSTF'RSLLEDDDMGDLVDAEEXLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055 | QY 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110  DD 514SRTPLLSSLSATSNNSATNCIDRNGQGHPVREDSFVQ 550 | QY 1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE 1168                        | Qy         1169 RAKTLSPGKNGVVKDVF | RESULT 12 TVYCH protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H) C.Species: avian erythroblastosis virus C.Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999 C.Accession: A00644, A38022 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. C.B. 135, 71-8, 1983 | A; Tille: Interior gene of avian erythiobiascosis vitus is a member of the sic gene family. A; Reference number: A00644; MUID:84026539; PMID:631329 A; Accession: A0064 A; Molecule type: DNA A; Residues: 1-604 < YAM> A; Cross-references: GB:K01216; NID:9209676; PIDN:AAA42400.1; PID:9209678 B; Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, Science 224, 1456-1459, 1984 A; Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of A; Reference number: A38022; MUID:84223957; PMID:6328658 | A,Wolecule type: DNA A,Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 <deb> A,Cross-references: GB:K02006 C,Generics: A,Cross-references: GB:K02006 C,Generics: A,Cross-references: GB:K02006 C,Generics: A,Cross-references: GB:K02006 C,Koywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific F;130-395/Domain: protein kinase homology <kin> F;130-395/Domain: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted</kin></deb>   |
|---|---|---|--|---|--|---|--|-----------------------------------|---|---|---|
| Db 761 VGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIAKGM 820 Qy 834 SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES 893 | OY 894 ILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM 953 | OY 954 IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1013    | QY 1014 MGDLVDAEFYLVPQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEE 1068  1014 MGDLVDAEFYLVPQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEE 1068  1014 MGDLVDAEFYLVPQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEE 1068  1014 MGDLVDAEFYLVPQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEE 1068  1014 MGDLVDAEFYLVPQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEE 1068 | QY 1069BAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD 1105<br>                   | QY 1106 PSFLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 1145                    | QY 1146 RPQPPSPRECPLPAARPAGATLERAKTLSP-GKNGVVKDVFAF 1187  | QY         1188 GGAVENPEYLTPQGGAAPQPHPP 1210           DD         1192EEYEYMNRKRRGSP-PRPP 1209 | kinase                            | hey, F.A.; GOOGWIN, K.G.; KOCTMAN, F.M.; Crittenden, L.B.; Kaines, PS 18 18 18 18 18 18 18 18 18 18 18 18 18  | I growth factor receptor; protein kinase homology is; phosphotransferase; transforming protein; tyrosine-specific pin (fragment) #status predicted <gags. #status="" (fragment)="" <env="" iein="" predicted=""> in-tyrosine kinase erbB #status predicted <erb> in kinase homology <kin> in kinase ATP-binding motif</kin></erb></gags.>   | Query Match         25.9%; Score 1766.5; DB 1; Length 698;           Best Local Similarity         52.2%; Pred. No. 1.2e-65;           Matches 374; Conservative 80; Mismatches 137; Indels 125; Gaps 18;           Qy         578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKPPDEBGACQPCPINCTHSCVDL 637           I |

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A;Residues: 'A', 832-866, 'V', 868-943, 'QTPSLVK' «WAD>
A;Residues: 'A', 832-866, 'V', 868-943, 'QTPSLVK' «WAD>
A;Cross-references: EMBL:X02293; NID:g7922; PIDN:CAA26157.1; PID:g929565
C;Comment: This sequence is tentative because the introns have not been identified.
C;Genetics:
A;Genes: EFPBase: Egfr
A;Genes: FlyBase: FlyBase: FBgn0003731
A;Map position: 2 57F
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein; phosphoposphorylation; duplication; glycoprotein; phosphoposphorylation; duplication; glycoprotein; phosphoposphorylation; duplication; glycoprotein; phosphoposphorylation; attacts predicted <EXT>
C;Superfamily: epidermal growth factor receptor; protein; phosphoposphorylation gredicted <INM>
F;1-732/Domain: extracellular #status predicted <INM>
F;33-764/Domain: protein kinase Hattus predicted <INM>
F;816-824/Region: protein kinase ATP-binding site: carbohydrate (Asn) (covalent) #status predicted
F;144/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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NiContains: protein-tyrosine kinaee (EC 2.7.1.112) etbB
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Sacession: A00640; A38021
R.Livneh, E.: Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Cell 40, 599-607, 1985
A.Title: The Drosophila EGF receptor gene homolog: conservation of both hormone bindi
A.Reference number: A00640; MUID:85124611; PMID:2982499
A.Accession: A00640
A.Molecule type: DNA
A.Residues: 1-130 cLIV>
A.Cross-references: EMBL:K03054
R.Madsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature 314, 178-180, 1985
A.Title: A Drosophila genomic sequence with homology to human epidermal growth factor
A.Reference number: A38021; MUID:85137938; PMID:2983232
A.Accession: A38021
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                                        126;
   Length 604;
                                       Indels
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25.0%; Scor
52.2%; Pred
                     Best Local Similarity 52.2
Matches 360; Conservative
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| Db 715 QYTAIGPYCAASPPRSSKITANLDVNMIFIITGAVLVPTIC  Qy 669 VVFGI-LIKRRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKV  15   | 755 Qy 638 725 Db 58 815 Qy 697 785 Ch 757  |
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| Db 816 LGMGAFGRUYKGVWVPEGENVKIPVAIKELLKSTGAESSEEFLREAYIMASEEHVNLLKL  Qy 786 LGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRD  Db 876 LAVCMSSQMMLITQLMPLGCLLDYVRNNRDKIGSKALLNWSTQIAKGMSYLEEKRLVHRD   | 174   EATSPRANGET   |
| OY 846 LAARNVLVKSPNHYKITDFGLARLLDIDETEYHADGGKVPIKWALESILRRRFTHO   | 902  Qy 877 YHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE 991  992  993  994  995  996  997  997  998  998  999  |
| OY 903 SDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMID   | 962 Qy 937 KGERLPOPPICTIDVYMIMVKCWMIDSECRPRELVSEFSRWARDPORFVIO-NEDLG 1051 Dia 1   |
| QY 963 SECRPRELVSEFSRMARDPQREVVIONEDLGPASPLDSTFYRSLLEDDDMGDL 1017   | Qy 996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSTRSG  |
| OY 1018 VDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSTRSGGGDLTLGLEPSEERAP Db 1105 TDGSEAIAKPDDYLQPKAALGFSHRTDCTDEMPKLNRYC   | 1071  Qy 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ   |
| QY         1072 RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV 1128           :  | 28 QY 1111 RYSEDPTVELPSETDGYVAPLTCSPQPEVVNQPDVRPQPPSPREGPLPAARPAGAT-LER 11  |
| OY 1129 APLTCSPQPEYVNOPDVRPQPPSPRGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188 Db 1183 MP-TCQPGPNNNNNMNNPNQNNMAAVGVAAGYMDLIGVP 1220   | Db 482PVREDGFLPPREDGFL 523 3 1188 Qy 1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197   |
| OY 1189 GAVENPEYLTPQGGAAPQPHPPPAFSP-AFDNLYYWD :   | 1224 DD 524 LPIDSRYQNSHSTAN<br>1279 RESULT 15   |
| RESULT 14 S35745 S15745 Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Date: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745 SK:Vennstroem, B. Submitted to the EMBL Data Library, March 1993 | kinaee-related transforming protein (erbB) (EC 2.7.1) - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997 C;Accession: S00727 |
| A.Molecule type: DNA<br>A.Residues: 1-544 <ven><br/>A.Cross-references: EMBL:X12707</ven>   |   |
| A;Gene: erbB<br>C;Superfamily: epidermal growth factor receptor; protein kinase homology<br>C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine<br>Fil35-400/Domain: protein kinase homology <kin></kin>  | -specific p   |
| Firston Filth Region: process Annual Motor Filth Annual Motor Filth Annual Motor Filth Annual Predicted   | Query March 24.1%; Score 1640; DB 2; Length 545; Best Local Similarity 54.9%; Pred. No. 1.4e-60; Matches 345; Conservative 69; Mismatches 122; Indels 92; Gaps 15;  |
| Query match<br>Best Local Similarity 54.9%; Pred. No. 7.3e-61;<br>Matches 345; Conservative 70; Mismatches 121; Indels 92; Gaps   | Oy 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637   |
| Qy 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL   | 637  Qy 638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQKIRKYTWRRLLGGTEL 57  Db 58 GLEGCP1GSKTPSIAAGVVGGLCLVVVGLGIGLYLRR-HIVRKPTLRRLLGEREL   |

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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues Her2'can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
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Birk P, Karlsson G;
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).

The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 corp. (CTL (Cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 corp. B-cell group derived from the PA; and (2) at least 1 contract T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial compart of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively. ö ELTYLPTNASLSFLODIOEVOGYVLIAHNOVROVPLORLRIVRGTQLFEDNYALAVLDNG 120 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180 300 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360 420 420 480 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540 9 900 9 9 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720 780 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120 DPLNNTTPVTGASPGGLRELOLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPQYIKANSK 240 FIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360 PWDOLFRNPHOALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTQCVNCSQFLRGQEC 540 1 MELAALCRWGLILALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60 VEECRVI.QGL.PREYVNARHCL.PCH.PECQPQNGSVT.CFGPEADQCVACAHYKDPPFCVARC RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAGVGSP 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV Gaps ö Length 1255; Indels DB 21; 13; 0; Mismatches Score 6704; Pred. No. 0; 98.7%; 99.0%; Query Match
Best Local Similarity 99.0
Matches 1242; Conservative 1255 AA; Sequence 241 241 61 61 121 181 181 301 361 361 421 481 541 601 661 721 121 301 421 481 541 601 661 721 g 8 g g d ð g 셤 ò g ò 요 ò g à g 8 ò 8 8 g ò 8 8

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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HBR-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present coffirm transduction of polynucleotides into host cells. The present of the invention are designed based on the HBR-2 antigenic peptide
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YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                    VSSRLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGMSYLEDVR
                                                                            LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
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                                                                                                                                                          HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI
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                        The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and pl85neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEI LDEAYVMAGVGSP
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                                                                YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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16-MAR-2000; 2000US-0189844.
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N-PSDB; AAF24297.
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is characterised by the overexpression of an epidermal growth factor receptor (BrbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB. The method is also useful for treating neuronal, glial, sstrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2)
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                                                      HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI M.
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           Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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                                                                                                                                                            Length 1255
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676..1255
/label Intracellular domain
/note= "Claimed domain, useful for immunisation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
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                                                                                                                                                  The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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   EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                            NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                        IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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| hemagglutinin-ne  | HNNZ80 |    | 572 | 51.4 | 38 | 45 |  |
|-------------------|--------|----|-----|------|----|----|--|
| methyl-accepting  | E82395 | 7  | 561 | 51.4 | 38 | 44 |  |
| cellulase (EC 3.  | T52135 | 7  | 501 | 51.4 | 38 | 43 |  |
| endo-1,4-beta glı | A86158 | 7  | 501 | 51.4 | 38 | 42 |  |
| hypothetical prof | T29127 | 0  | 424 | 51.4 | 38 | 41 |  |
| hypothetical prof | T51466 | α. | 383 | 51.4 | 38 | 40 |  |
| probable hexosylt | F71196 | 7  | 381 | 51.4 | 38 | 39 |  |
| tRNA-pseudouridi  | F70361 | ~  | 287 | 51.4 | 38 | 38 |  |
| hypothetical prof | F64472 | 7  | 256 | 51.4 | 38 | 37 |  |
| hypothetical pro  | A64639 | 7  | 188 | 51.4 | 38 | 36 |  |
| hypothetical pro  | H71875 | 7  | 188 | 51.4 | 38 | 35 |  |
| hypothetical pro  | C90269 | ~  | 505 | 52.7 | 39 | 34 |  |
| type IIS restrict | F64690 | 7  | 423 | 52.7 | 39 | 33 |  |
| probable acetyl-( | T43043 | ~  | 349 | 52.7 | 39 | 32 |  |
| type II restricti | B71808 | ~  | 326 | 52.7 | 39 | 31 |  |
| adenylate kinase  | KIYMC  | н  | 213 | 52.7 | 39 | 30 |  |

|   | 30           | 39        | 52.7  | 213             | н.         | KIYMC                   | adenylate kinase (   |
|---|--------------|-----------|---|-----------------|------------|-------------------------|--|
|   | 31           | 9.        | 52.7  | 326             |            | B.71808                 | type il restrictio   |
|   | 32           | 66        | 52.7  | 349             | ~ (        | T43043                  | probable acetyl-co   |
|   | E .          | ر<br>د د  | 52.7  | 423             | 7          | F64690                  | Sec  |
|   | 34           | 66        | 52.7  | 505             | N (        | C90269                  |  |
|   | 35           | 38        | 51.4  | 188             | 7          | H71875                  |  |
|   | 36           | 38        | 51.4  | 188             | 7          | A64639                  | hypothetical prote   |
|   | 37           | 38        | 51.4  | 256             | 7          | F64472                  | hypothetical prote   |
|   | 38           | 38        | 51.4  | 287             | ~          | F70361                  | tRNA-pseudouridine   |
|   | 39           | 38        | 51.4  | 381             | 7          | F71196                  | probable hexosyltr   |
|   | 40           | 38        | 51.4  | 383             | ~          | T51466                  | hypothetical prote   |
|   | 4            | 38        | 51  | 424             | .۵         | T29127                  | hypothetical prote   |
|   | . 4          | 80 6      | 4   | 501             | ۱ ۸        | A86158                  | endo-1.4-beta gluc   |
|   | 7 7          | ) c       | . 4   | נטג             | ۰,         | T52135                  | cellulase (EC 3.2.   |
|   |              | ם<br>מ    |   |                 | 1 (        | T02220                  | methy] - accepting   |
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|   | N.Alternal   | משבר סד   | 1 4 4 1   | שת פווחה        | 11170      | toxin                   |  |
|   | C:Species    | Clost     | ridium  | tetani          |            |                         |  |
|   | C.Date       | 1-Mar-1   | 988 #8  | egnence         | re         | vision 31-Mar-          | -1988 #text change 03-Jun-2002                             |
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|   | EMBO 1       | 2495-     | 2502  | 1986            | ,          | (iv (iv)                |  |
|   | A:Title:     | Tetanus   | toxin   | r orima         | 2          | structure, ex           | pression in E. coli. and homology with botul               |
|   | A:Referen    | de numb   | Der: A2   | 5689: N         |            | :87053814: PM1          | 16   |
|   | A: Accession | A25       | 689   |                 |            |                         |  |
|   | A:Molecul    | type:     | DNA   |                 |            |                         |  |
|   | A.Regidue    | 113       | 115 <rt< td=""><td>S.</td><td></td><td></td><td></td></rt<>     | S.              |            |                         |  |
|   | A, Acetade   | of orong  | 197 .00   | . YOAA36        | 2          | TTG . 037042. GT        | 0770A2.010 1. DID: 040770                                  |
|   | A;CIOSB-I    | thorem.   | 15 . E  | : A04456        | 4 6        | 1D:840/07; F11          |  |
|   | K, Fallwea   | cher, r   | 1   | yness,          | > 0        |                         |  |
|   | Nucleic A    | cids Ke   | . 14,   | ,-608/          | 81.        | 1986                    |  |
|   | A;Title:     | The con   | nplete  | nucleot         | 196        | sequence of t           | tetanus toxin.   |
|   | A;Referen    | ce num    | ber: A2   | 5757;           | TI CI      | :87040747; PM           | ID:3774547   |
|   | A; Accessi   | on: A25   | 5757  |                 |            |                         |  |
|   | A; Molecul   | e type:   | DNA   |                 |            |                         |  |
|   | A;Residue    | 8: 1-13   | 315 <fa< td=""><td>í,</td><td></td><td></td><td></td></fa<>     | í,              |            |                         |  |
|   | A;Cross-r    | eferenc   | ses: GB   | 1:X06214        | -          | ID:940773; PII          | PIDN:CAA29564.1; PID:g40774                                |
|   | A; Experim   | ental E   | source:   | strair          | į.         | 3911                    |  |
|   | R, Fairwea   | ther, N   | 4.F.; L   | yness,          | >          | .; Pickard, D.          | .J.; Allen, G.; Thomson, R.O.                              |
|   | J. Bacter    | iol. 16   | 55, 21-   | 27, 198         | 9          |                         | •  |
| - | A; Title:    | Cloning   | <pre>j, nucl</pre>  | eotide          | seo        | uencing, and $\epsilon$ | expression of tetanus toxin fragment C in E                |
|   | A;Referen    | ce numk   | ber: A2   | 5194; N         | III.       | :86085672; PM           | ID:3510187   |
|   | A; Accessi   | on: A25   | 5194  |                 |            |                         |  |
|   | A; Molecul   | e type:   | DNA   |                 |            |                         |  |
|   | A; Residue   | 8: 743-   | -1315 <   | FA2>            |            |                         |  |
|   | A; Cross-r   | eferenc   | Jes: GB   | 1:M12735        | 2          | ID:q144920; P1          | PIDN: AAA23282.1; PID: 9144921                             |
|   | A; Accessi   | on: B25   | 5194  |                 |            | 1                       |  |
|   | A; Molecul   | e type:   | : prote   | iin             |            |                         |  |
|   | A;Residue    | 8:865-    | -894 <f< td=""><td>'A3&gt;</td><td></td><td></td><td></td></f<> | 'A3>            |            |                         |  |
|   | R;Matsuda    | , M.,     | Lei, D.   | L.; Suç         | 1 mc       | to, N.; Ozutsı          | umi, K.; Okabe, T.   |
|   | Infect. I    | mmun. F   | 57, 358   | 18-3593,        | 13         | 89                      |  |
|   | A;Title:     | Isolati   | ion, pu   | rificat         | ior        | , and characte          | erization of fragment B, the NH-2-terminal                 |
|   | A;Referen    | ce numb   | oer: A6   | 0759; N         | UIL        | :90035436; PM]          | ID:2478476   |
|   | A; Accessi   | on: A60   | 1759  |                 |            |                         |  |
|   | A, Molecul   | e type:   | : prote   | nin             |            |                         |  |
|   | A, Residue   | B: 461-   | -475 <m< td=""><td>IAT&gt;</td><td></td><td></td><td></td></m<> | IAT>            |            |                         |  |
|   | R; Demotz,   | S.; Le    | anzavec   | chia, I         |            | Eisel, U.; Nie          | emann, H.; Widmann, C.; Corradin, G.                       |
|   | J. Immuno    | 1. 142,   | . 394-4   | 02, 198         | 9          |                         |  |
|   | A; Title:    | Deline    | ation o   | f sever         | al         | DR-restricted           | tetanus toxin T cell epitopes.                             |
|   | A;Referen    | ce numk   | oer: JS   | 1 :6000         | ĮĮ.        | :89093918; PM           | A; Reference number: JS0098; MUID: 89093918; PMID: 2463305 |
|   | A; Content   | B: annc   | otation   | 1, epitc        | <u>α</u> , | region                  |  |
| _ | R; Schiavo   | 9.5       | Sentena   | ti, F.,         | 2          | ulain, B.; Ros          | ssetto, O.; de Laureto, P.P.; DasGupta, B.R                |
|   | Nature 35    | 9, 832-   | -835, 1   | .992            | ,          |                         |  |
|   | A;Title:     | Tetanus   | and b   | otulini<br>Sigi | 14-E       | neurotoxins I           | block neurotransmitter release by proteolyti               |
|   | A; Reteren   | ce num    | oer: 52   | 7125;           | ĮĮ į       | :93063293; PM.          | A,Reterance number: 52/12>; MUID:93063293; PMID:133180/    |
| - | A; concent   | alling:   | J. a. L. D.   | _               |            |                         |  |

If heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r Ig heavy chain V r conserved hypothet

[acyl-carrier-prot oligopeptidase (EC oligoendopeptidase

hypothetical prote

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N.Alternate names: spermidine acetyltransferase
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C;Accession: G86826
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssgl A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lactis
           sequence was submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: yqfF
C;Superfamily: Escherichia coli ribosomal-protein-alanine N-acetyltransferase rimJ
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A,Cross-references: GB:AE005176, PID:g12724622; PIDN:AAK05713.1, GSPDB:GN00146
A,Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 63 - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A,Description: Primary structure of the herpesvirus ateles genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 899;
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A;Molecule type: DNA
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A;Experimental source: strain 73
                                                                                                                                                     DB 2;
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Pred. No. 13;
1; Mismatches
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                                                                                                                                                        Score 44;
Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: acyltransferase; coenzyme A
                                                                                                                                                     59.5%;
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64.3%;
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124 QYITSNSTFTGQTE 137
                                                                                                                                                                                                                                                                     2 YIKANSKFIGITEL 15
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50 YIKRNGKFVGTWEV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OYIKANSKFIGITE 14
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Best Local Similarity 64...
Best Local Similarity 64...
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Matches 9: Conservative
                                                                                                                                                                                                                8; Conservative
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Best Local Similarity
Matches 8; Conserv
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           nucleotide
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A;Molecule type: DNA
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                                                                                              GIG
                                      C;Genetics:
A;Gene: 84
A;Start codon: G
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Ride Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C. Bur. J. Biochem. 229, 61-69, 1995

Far. J. Biochem. 229, 61-69, 1995

Faritie: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin. A; Reference number: S69348; MUID:95262688; PMID:7744050

A; Rocession: S69348

A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: protein

A; Residues: 2-31 cDEF.

C; Comment: The source of this protein was an extrachromosomal plasmid.

C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B); Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized c; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                                                                                                                                                                                                                                                                                                                                                                         C.Function:
Albescription: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt
C.Superfamily: tetanus toxin
C.Superfamily: tetanus toxin
C.Superfamily: tetanus toxin
C.Superfamily: tetanus toxin
C.Superfamily: tetanus toxin
C.Superfamily: tetanus toxin
E.2457/Product: tentoxylysin light chain (fragment A) #status predicted TIL>
F.2457/Product: tentoxylysin heavy chain (fragment B) #status experimental TTH>
F.461-1315/Product: tentoxylysin beavy chain (fragment B) #status predicted <TXB>
F.865-1315/Domain: channel forming (fragment C) #status predicted <TXC>
F.233,237/Binding site: zinc (His) #status predicted
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C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: 531029
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans A;Reference number: S30949; MUID:93211283; PMID:8459767
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class II histocompatibility antigen - Atlantic salmon
C;Species: Salmo salar (Atlantic salmon)
C;Date: Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: $29982
R;Hordvik, I.
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A;Cross-references: EMBL:X70166; NID:g64369; PID:g64370
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
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submitted to the EMBL Data Library, October 1992
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EYIRFNSTVGKFVGYTEL 68
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Matches 10, Conservative
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A;Accession: S29982
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Best Local Similarity
Matches 15; Conserva
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A;Molecule type: mRNA
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Query Match

ઠ 요 RESULT

A;Cross-references: EMBL:Z18946; NID:g15859; PIDN:CAA79460.1; PID:e59702; PID:g579152

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Gaps

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Indels

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A; Molecule type: DNA
A; Mesidues: 1-1104 <WEB1>
A; Cross-references: EMBL:X03831
R; Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 138
A; Title: Merozoite surface protein sequence from the Camp strain of the human malaria pa;
A; Reference number: S06361; MUID:88143999; PMID:3278296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Comment: The merozoite stages of different strains have strain-specific surface antiger C, Comment: The merozoite stages: sporozoite, merozoite, and gametocyte. The mero C, Superfamanly: major merozoite surface antigen (S, Superfamanly: major merozoite; surface antigen (S, Stay Mords: g) y coprotein; merozoite; surface antigen, tandem repeat (S, P, 1-19/Domain: signal sequence #status predicted <SIG> (S, P, 1-76/Product: major merozoite surface antigen #status predicted <MAT> (S, P, 100-105, 109-120/Region: 3-residue repeats (S-G-T) (S, 107-105, 109-120/Region: 3-residue repeats (T-E-E) (S, 113, 272, 501, 567, 638, 827, 839, 924, 944, 990, 1016, 1114, 1221, 1613, 1658/Binding site: carbohyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st)
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N;Alternate names: 195K glycoprotein
C;Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Plasmodium falciparum
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1701/Product: major merozoite surface antigen #status predicted
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R;Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. Biol. 195, 273-287, 1987
A;Title: Allelic dimorphism in a surface antigen gene of A;Reference number: A26868; MUID:88011243; PMID:3079521
A;Accession: A26868
                                                                           DB 2;
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                                                                                                                                                          4; Mismatches
                                                                      57.4%; Score 42.5; 60.0%; Pred. No. 30;
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A;Residues: 1-1701 <TAN>
C;Superfamily: major merozoite surface antigen
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1001 QFVKSNSKVITGLTE 1015
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                                 Ouery Match
Best Local Similarity 60.07
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A, Residues: 1104-1726 <WEB2>
C; Keywords: surface antigen
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Matches
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A26868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Major Merozoite surface antigen MSA-1 - malaria parasite (Plasmodium falciparum) (fragme major merozoite surface antigen MSA-1 - malaria parasite (Plasmodium falciparum) (fragme NA1ternate names: polymorphic schizont antigen p190 (S.Species: Plasmodium falciparum (S.Species: Plasmodium falciparum (S.Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000 (S.Species) (M.S.Species) (M.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASSAUSE

Major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (is

C.Species: Plasmodium falciparum

C.Species: Plasmodium falciparum

C.SACCESSION: AS4498

R.Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.;

M.O.: Biochem. Parasitol. 27, 291-302, 1988

A.Title: Variation in the precursor to the major merozoite surface antigens of Plasmodiu

A.Reference number: AS4498; MuID:88142999; PMID:2449612

A.Status; preliminary
                                     (Bt
                                                                                                                                                                                                                                                                                                                         surface antigen precursor p190 of
                         major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
NyAlternate names: 190K protein; polymorphic schizont antigen
C;Species: Plasmodium falciparum
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000
C;Accession: 206286
R;Certa, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.
EMBO J. 6, 4137-4142, 1997
A;Title: A naturally occurring gene encoding the major surface antigen precursor pl90
A;Reference number: 506286; MUID:88166657; PMID:3327688
A;Accession: 506286
A;Accession: Compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
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*Residues: 1-1701 <PET>
A;Cross-references: GB:M19143; NID;g160412; PIDN:AAA29653.1; PID:g160413
C;Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: MSAl
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1060;
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60.0%; Pred. No. 19;
iive 4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.5; DE Pred. No. 19; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reaidues: 1-1060 <CER>
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1009 QFVKSNSKVITGLTE 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.4%;
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983 QFVKSNSKVITGLTE 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QYIKANSKFI-GITE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QYIKANSKFI-GITE 14
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A;Cross-references: EMBL:X61930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
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of the malaria parasite Plasmodium

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diderophore/Surfactin synthetase related protein [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Sate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: H97146
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Barton, G.; M.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001437; PIDN:AAK79963.1; PID:g15024986; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C;Accession: G36812
R;Albrecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, January 1992
A.Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806
A;Accession: G36812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ORF63 - saimiriine herpesvirus 1 (strain 11)
                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-123 <TAS3
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 447;
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Pred. No. 30;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                    Score 41; DB :
Pred. No. 3.9;
                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                 55.4%;
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                                                                                                                                                                                                                                                                                                                     2 YIKANSKFIGITEL 15
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                                                                                                                                                                                                                                       Best Local Similarity 64.3
Matches 9; Conservative
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291 KYIRTNKKFIG 301
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Best Local Similarity
Matches 7; Conserv
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Best Local S:
Matches 7
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                                                                                                                                                                                                                              major merozoite surface antigen precuxsor - malaria parasite (Plasmodium falciparum) (st
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C;Accession: A45948
R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A;Reference number: A45948, MuID:89005525; PMID:3049134
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Ig heavy chain V-D-J region (419.1) - mouse (fragment)

C;Species: Ms musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: 648677

R;Tassignen, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C

R;Tassignen, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C

R;Tassignen, J.; Brait, M.; Jamila, I.; Wrbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C

R;Tatle: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodie

A;Reference number: A48677; MUID:94022404; PMID:8415731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
538635
blastopia polyprotein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S38635
R;Frommer, G.; Schuh, R.; Jdckle, H.
submitted to the EMBL Data Library, November 1993
A;Description: Localized expression of a novel micropia-like element in the blastoderm A;Reference number: S38635
A;Accession: S38635
A;Status: preliminary
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Pred. No. 29;
     Indels
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A;Residues: 1-1333 <FRO>
A;Cross-references: EMBL:Z27119; NID:9415797; PID:9415798
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Mismatches
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3; Mismatches
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A, Molecule type: DNA
A, Residues: 1-1726 < CHA>
A, Crose-references: GB: M37213
C, Superfamily: major merozoite surface antigen
C, Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: FlyBase:micropia
A;Cross-references: FlyBase:FBgn0014947
C;Keywords: polyprotein
     4
                                                                                                 1026 OFVKSNSKVITGLTE 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 56.8%;
Local Similarity 53.3%;
les 8; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
9; Conservative
                                                   1 QYIKANSKFI-GITE
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1 QYIKANSKFIGITE 14 ||| :|| ||::| 124 QYITSNATFTGLSE 137

Search completed: July 22, 2003, 08:12:43 Job time : 2.75523 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Shumin Z., Dianliang L.;
Shumin Z., Dianliang L.;
Shumited dura-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF389424; AAK72964.2;
InterPro; IPR000395; Bontcoxilysin.
InterPro; IPR000130; Zn MTpeptdse.
PERM; PERM; PERM; PERM; J. PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; PERM; 
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2002 (TrEMBLrel. 20, Last annotation update)
Tetanus toxin (Fragment).
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                                                                                 Q255922
Q8TZU8
Q24262
Q9DEK4
Q951S3
Q951S3
Q951S3
Q96JH0
Q9GJH0
Q9GJG9
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Q9HD07
Q8RCF9
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Q9DEJ6
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Q31577
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0951S6
0951S5
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Q31582
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nes 15; Conservative
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42.5
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Matches
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Q93N27
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Q9xxj9 salvelinus
Q95xs2 salmo salar
Q95hy4 salmo salar
Q31590 salmo salar
Q31579 guillardia
Q31578 salmo salar
Q9cf66 lactococcus
Q9mc1 farreptococcus
Q9mc1 farreptococcus
Q9xje8 lactococcus
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Q9cyd2 mus musculu
Q9ytk4 ateline her
Q25961 plasmodium
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                                                                                                                                                                                                July 22, 2003, 08:05:49; Search time 1.51046 Seconds (without alignments) 2046.206 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671580
                            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             OM protein - protein search, using sw model
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Q31585
Q9XRJ9
Q95RJ9
Q95HY1
Q95HX4
Q31590
Q9XG37
Q9XG37
Q9XG37
Q9XG37
Q9XG37
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Q9CYD2
Q9YTK4
Q25961
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Gapop 10.0 , Gapext 0.5
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sp bacteria:*
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sp_vertebrate:*
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Maximum DB seq length: 200000000
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Match Length DB
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Result Š ö

Gaps

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SECUENCE FROM N.A.

Landry C., Bernatchez L.;

Comparative analysis of population structure across environments and geographic scales at Major Histocompatibility Complex and microsatellite in Atlantic salmon (Salmo salar).";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MHC class II beta chain (Fragment).
Salmo salar (Atlantic salmon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Taleostoi; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmo salar (Atlantić salmon).
Wataryota; Metazoda; Chordata; Caraniata; Vertebrata; Buteleostomi; Actinopterygii, Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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"Allelic polymorphism in WHC class II B in four populations of Atlantic salmon (Salmo salar).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.5; DB 7; Length 85;
Pred. No. 2.2;
3; Mismatches 2; Indel8
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Pred. No. 2.2;
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85 AA; 9723 MW; 27C9F7931F1F01C4 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MHC class II B antigen (Fragment).
                       85 AA
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MEDLINE=21383619; PubMed=11491536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenetics 53:329-336(2001).
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 10, Conservative
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Matches 10; Conservative
                       PRELIMINARY;
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Q95HY1
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"A study of polymorphism in the MHC class II beta 1 and MHC class alpha 2 domain exons of Atlantic salmon (Salmo salar).";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L24953; AAA49597.1;
InterPro; IPR0010353; MHC II beta.
Pfam; PF00569; MHC II beta.
Probom; PD000328; MHC II beta.
Probom; PM000328; MHC II beta.
Probom; PM000328; MHC II beta.
Propom; PM000328; MHC II beta.
                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(DB02) MHC class II bera 1 (Fragment).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Proteacanthopterygii, Salmoniformes, Salmonidae, Salvelinus.
NCBI_TaxID=8040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dorschner M.O., Duris T., Phillips R.B.;
"Diversity of a Lake Trout Mhc class II Gene.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR130026; AAD20889-1; --
INTERPORT MAD20889-1; --
INTERPORT MHC II beta.
Pfam; PF00969; MHC II beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5D4F3449060940E2 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Glycoprotein; MHC II; Transmembrane.
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PRT;
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55.6%;
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Best Local Similarity 55.6%;
Matches 10; Conservative
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60.1%; Score 44.5; DB 7; Length 244; 55.6%; Pred. No. 6.4; ive 3; Mismatches 2; Indels
      SMART; SM00407; IGC1; 1.
Glycoprotein; MHC II; Transmembrane.
SEQUENCE 244 AA; 27449 MW; 496CB9EA9D73765C CRC64;
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Best Local Similarity 50.0%,
A Conservative
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445 FIKSNSRFMRLTEI 458
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MEDLINE=93170890; PubMed=8436418;
MEDLINE=93170890; PubMed=8436418;
Hordvik I., Grimholt U., Posse V.M., Lie Y., Endresen C.;
"Cloning and sequence analysis of cDNAs encoding the MHC class II chain in Atlantic salmon, Salmo salar.";
Immunogenetics 37:437-441(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21383619; PubMed=11491536;
Langefors A., Lohm J., von Schantz T.;
"Allelic polymorphism in MHC class II B in four populations of
Atlantic salmon (Salmo salar).";
Immunogenetics 53:329-336(2001).
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                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
MHC class II B antigen (Fragment).
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InterPro.; PPR00053; MHC II beta.
Pfam, PF00969; MHC II beta; II.
ProDom; PD000328; MHC_II_beta; II.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003033; MHC_II_beta.
Pfam; PF0047; ig; I_beta; I.
Pfam; PF00969; MHC_II_beta; I.
ProDom; PD000328; MHC_II_beta; I.
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33 EYIRFNSTVGKFVGYTEL 50
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MHC-SASA CLASS II B.
Salmo salar (Atlantic salmon).
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33 EYIRFNSTVGKFVGYTEL
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE FROM N.A.
MEDLINE=20087226; PubMed=10618395;
Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
Cavalier-Smith T., Maier U., Douglas S.,
"Chloroplast protein and centrosomal genes, a tRNA intron, and odd
telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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EMBL; L24929; AAA49550.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21223349; PubMed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L., Wu X., Reith M., Cavalier-Smith T., Maier U.;
"The highly reduced genome of an englaved algal nucleus.";
Nature 410:1091-1096(2001).
Hypothetical protein.
SEQUENCE 546 AA; 66218 MW; 7303950F632BE6F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmo salar (Atlantic salmon).
Wataryota; Metacoa; Chordata; Caniata; Vertebrata; Buteleostomi; Actinopterygii, Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                               Eukaryota, Cryptophyta, Cryptomonadaceae, Guillardia.
NCBI_TaxID=55529;
                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 66.2 kDa protein.
Guillardia theta (Cryptomonas phi).
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546 AA.
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SEQUENCE FROM N.A.
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Q9XJE8
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09CRV4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=20088830; PubMed=10620678;
Stanläy E., Walsh L., van der Zwet A., Fitzgerald G.F.,
van Sinderen D.;
"Identification of four loci isolated from two Streptococcus
"Identification of four sesponsible for mediating bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus thermophilus bacteriophage 7201.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=112023;
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                                                                                                                                                              Score 43.5; DB 7; Length 67;
Pred. No. 2.6;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6DBD148524C0DF3C CRC64;
                                                                                                                        67 AA; 7449 MW; 42771AEDBABA6626 CRC64;
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Last annotation update)
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                   Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC II beta; 1.
Glycoprotein; MHC II; Transmembrane.
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InterPro; IPR000353; MHC II beta,
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Transferase, Complete proteome.
eronmance 180 AA, 21022 MW; 6
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16 EYVRFNSTVGKFVGYTEL 33
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NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
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Best Local Similarity 69.4
Best Local 9; Conservative
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65 IEANDTFIGIVEL 77
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les 9; Conservative
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SEQUENCE
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Q9CF66
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van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.; "Molecular analysis of the temperate lactococcal phage Tuc2009."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Lactococcus lactis bacteriophage Tuc2009.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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Pred. No. 12;
                                                                       Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF145054; AF4743506.1; -AF4743506.1; -AF4743506.1; -InterPro; IPR001091; CN4 Metransf. InterPro; IPR001295; D2ING mtfrase. InterPro; IPR002295; D2ING mtfrase. InterPro; IPR002295; N6/N4 Mtase. PFam; PF01555; N6 N4 Mtase; 1. PR01555; N6 N4 Mtase; 1. PR01555; N6 N4 Mtase; 1. PR01555; N6 N4 Mtase; D2INGWTFRASE. PR0155; PR00508; S2INGWTFRASE.
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                                                                                                                                                                                                                                                                                                                           250 AA; 28744 MW; 725EA3B2B56B0D7F CRC64;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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FEMS Microbiol. Lett. 182:271-277 (2000)
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InterPro; IPR001091; CNA Metransf.
InterPro; IPR002295; D21M6 mtfrase.
InterPro; IPR002941; N6/N4 mtase.
Pfam; PF0155; N6 N4 mtase.
PRINTS; PR00506; D21M6WTFRASE.
PRINTS; PR00506; B21N6WTFRASE.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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57.1%;
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Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 8; Conservative
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                                                                         Rawai T., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A.; Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A.; Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Massdelland T., Gissi C., King B., Kochiwa H., Rastel K., Masslend T., Gissi C., King B., Kochiwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Warsho T., Ratal K., Towita M., Wagner L., Warsho T., Ratal K., Dolunga N., Carninci P., de Bonaldo M.F., Sakai K., Defini D., Bojunga N., Carninci P., de Bonaldo M., Lee N.H., Bulte J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M., Lee N.H., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzaralli J., Mombaerts P., Asakaki H., Sato K., Stochada M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Stochada K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski Y., Ramiski A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Remell, Akultonia annotation of a full-length mouse cDNA collection."; Remell. Akultonia annotation of a full-length mouse cDNA collection."; Remell Akulta M. Remell. Akulta M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Remell M., Rem
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MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-21085660; PubMed-11217851;

MARAWA J., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Madota K., Marsuda H.A., Ashburner M., Baralov S., Casavant T.,

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Manna M., Gasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
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PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS01179; PID; 1.
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                            STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
MEDLINE=21085660; PubMed=11217851;
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InterPro; IPR002086; Aldehyde dehydr.
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Pfam; PF00640; PID; 1.
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Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmig L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Pred. No. 15;
3; Mismatches 3; Indels
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Pred. No. 44;
1; Mismatches 4; Indels
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Albrecht J.-C., Fleckenstein B.;
Submitted (AUG-199) to the EMBL/GenBank/DDBJ databases.
EMBL, AF0934241, AAC95587.1; -.
SEQUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;
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MEDLINE=20091363; PubMed=10623770;
Albrecht J.C.;
"Primary structure of the Herpesvirus Ateles genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                            35272 MW; 535DD8E733C0F406 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                      MGD; MGI:1117926; 5710529006Rik.
InterPro; IPR0020508; Aldahyde dehydr.
InterPro; IPR000050; PID_domain.
Pfam; PF00640; PID; 1.
SMART; SM00462; PTB; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS010179; PID; 1.
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EMBL; AK017798; BAB:0939.1; -.
HSSP; Q02410; 1AQC.
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57.1%;
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64.3%;
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Best Local Similarity 64.3.
Local 9; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 22, 2003, 08:05:43; Search time 0.395043 Seconds (without alignments) 1574.881 Million cell updates/sec Run on:

US-09-806-703A-12 74 1 QYIKANSKFIGITEL 15

Title: Perfect score: Sequence:

BLOSUM62. Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                | clostric |      |      | P13819 plasmodium | P08569 plasmodium |            |            | _          | Q8rcf9 thermoanaer | Q01055 herpesvirus |            |            | Q9cev7 lactococcus |            | P10251 mycoplasma | Q58778 methanococc | O66922 aquifex aeo |            | haemo      |            | mus m      | P27115 oryctolagus |          |            | ģ          |            | Q10428 schizosacch | _          | chlamydi |      | O57383 xenopus lae |            | P19077 rhodobacter |
|-----------|----------------|----------|------|------|-------------------|-------------------|------------|------------|------------|--------------------|--------------------|------------|------------|--------------------|------------|-------------------|--------------------|--------------------|------------|------------|------------|------------|--------------------|----------|------------|------------|------------|--------------------|------------|----------|------|--------------------|------------|--------------------|
|           |                |          |      |      |                   |                   |            |            |            |                    |                    |            |            |                    |            |                   |                    |                    |            |            |            |            |                    |          |            |            |            |                    |            |          |      |                    |            |                    |
| SUMMARIES | ID             |          |      | 1    |                   |                   | MSP1_PLAFC | MSP1_PLAFP | PYRC_SERMA | LE12_THETN         | V120_HSVSA         | ACPD_HAEIN | PEF1_LACLC | PEPF_LACLA         | YHJ9 YEAST | KAD_MYCCA         |                    | TRUB AQUAE         | HEMA_PI3HT | Y096_HAEIN | GNT1 HUMAN | GNT1_MOUSE | GNT1_RABIT         | GNT1_RAT | Y032_BORBU | G6PD_ASPNG | G6PD_EMENI | YDD2_SCHPO         | Y358_BUCAI | ( )      |      |                    | MURD_BACSU | NIFN_RHOCA         |
|           | DB             | н        | Н    | Н    | Н                 | Н                 | н          | Н          | Н          | Н                  | Н                  | Н          | Н          | -                  | -1         | m                 | Н                  | Н                  | -          | Н          | -          | -          | -                  | Н        | -          | Н          | -          | -                  | -          | Н        | П    | П                  | -          | ۲                  |
|           | Length         | 1314     | 99   | 1682 | 1701              | 1701              | 1726       | 1726       | 204        | 384                | 899                | 194        | 601        | 601                | 644        | 213               | 256                | 287                | 572        | 191        | 445        | 447        | 447                | 447      | 490        | 510        | 511        | 548                | 169        | 258      | 296  | 333                | 451        | 461                |
| de        | Query<br>Match | 0        | 59.5 | 57.4 | 57.4              | 57.4              | 57.4       | 57.4       |            |                    | S                  |            | 4          |                    | 4          | 52.7              | 51.4               | 51.4               | 51.4       | 20.0       | 50.0       | 20.0       | 50.0               | 20.0     | 20.0       | 20.0       | 20.0       | 50.0               | 48.6       | 48.6     | 48.6 | 48.6               | 48.6       | 48.6               |
|           | Score          | 74       | -44  | 42.5 |                   |                   | 42.5       |            | 41         | 41                 | 41                 | 40         | 40         | 40                 | 40         | 39                | 38                 | 8                  | 38         | 37         | 37         | 37         | 37                 | 37       | 37         | 37         | 37         | 37                 | 36         | 36       | 36   | 36                 | 36         | 36                 |
|           | Result<br>No.  |          | α,   | m    | 4                 | Ŋ                 | φ          | 7          | 60         | σ                  | 10                 | 11         |            | 13                 |            | 15                | 16                 | 17                 | 18         | 19         | 20         | 21         | 22                 | 23       | 24         | 25         | 56         | 27                 | 28         | 29       | 30   | 31                 | 32         | 33                 |

| P11410 pichia jadi<br>P40009 saccharomyc<br>P21770 influenza c<br>P13877 influenza c<br>P04932 plasmodium<br>P04933 plasmodium<br>Q9731 spinacia ol<br>Q9741 clostridium<br>Q8764 salmonella<br>P04354 gallus gall<br>P13652 escherichia<br>Q10494 schizosacch  |
|---|
| GGED PICCJA<br>YND1_YEAST<br>RRP3_INCBE<br>RRP3_INCJJ<br>MSP1_PLAFW<br>MSP1_PLAFW<br>MUGC_SPIOL<br>ACD2_CLOAB<br>ACPD_SALTY<br>CADV_CHICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD_ECOLICK<br>CDD |
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### ALIGNMENTS

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59.5%;
                      829 QYIKANSKFIGITEL 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-1061 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hatfull G.F., Sarkis G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 YİKRNGKFVGTWEV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                               STANDARD;
                                                                                                                                                                                                                                     Gene 84 protein (GP84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831029;
                                                                                                                        VG84 BPML5
Q05301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                           G84 BPML5
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                     NAC. Struct. Biol. 4:788-792(1997).

-!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES. IS INTERNALIZED

AND MOVES BY RETYGGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPSEPTIDASE THAT CARALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77

BOND OF SYNAPTOBREVIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE AND ARE NON-TOXIC AFTER SEPARATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00760; BONTOXIIYSIN.
ProDom; PD001963; BONTOXIIYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
                                     IDENTIFICATION OF SUBSTRATE.
MEDLINE=93063293; PubMed=1331807;
SChiavo G., Benfennati F., Poulain B., Rossetto O., de Laureto P.P.,
Dasgupta B.R., Montecuco C.;
"Tetanus and botulinum-B neurotoxins block neurotransmitter release
by proteolytic eavage of synaptobrevin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                         Jmland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN- |-PHE-77 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO GANGLIOSIDE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 74; DB 1; Length 1314; 100.0%; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                               "Structure of the receptor binding fragment HC of tetanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; 134C3657133EF81D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETANUS TOXIN LIGHT CHAIN. TETANUS TOXIN HEAVY CHAIN.
                                                                                                                                                                                                                 OF 874-1314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=97475217; PubMed=9334741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000395; Bontoxilysin.
InterPro, IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X04436; CAA28033.1; -. EMBL; M12739; AAA23282.1; -.
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EMBO J. 11:3577-3583 (1992)
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Best Logal Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1AF9; 29-APR-98.
PDB; 1A8D; 14-OCT-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNAPTOBREVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; M27.001;
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INIT MET
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                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence, structure and gene expression of mycobacteriophage L5: a phage system for mycobacterial genetics."; Mol. Microbiol. 7:395-405(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-88166657; PubMed=3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen
precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSPI_PLAF3 STANDARD, PRT; 1682 AA.
P19598; Q25921;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tolle R., Bujard H., Cooper J.A.; "Plasmodium falciparum: variations within the C-terminal region of
                                                                                                                                                                     Mycobacteriophage L5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate ro-33 / Ghana).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 66; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S31029.
5 AA: 7424 MW; 9C7104C7A4FA74AS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
PRT;
                                                                                                                                                                                                                                                                                                                      MEDLINE=93211282; PubMed=8459766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exp. Parasitol. 81:47-54(1995)
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QYIKANSKFIGITEL 15

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                                      PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GPI-anchor.
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Peterson M.G., Coppel R.L., McIntyre-P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.;
"Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum."; Mol. Biochem. Parasitol. 27:291-302(1988). -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor 01-JNN-1990 (Rel. 13, Created) 01-JNN-1990 (Rel. 13, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Merozoite surface protein 1 precursor (Merozoite surface antigens) Plasmodium falciparum (isolate FC27 / Papua New Guinea). Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBL\_TaxID=5837; PRT; 1701 AA. SEQUENCE FROM N.A. MEDLINE=88142999; PubMed=2449612; |::|:||| | |:|| 983 QFVKSNSKVITGLTE 997 STANDARD; (Potential) PLAFF (PMMSA) RESULT 4
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88011243; PubMed=3079521;
Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-115 FROM N.A.

MEDLINES #66136024; PubMed=3104972;

Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,

Stunnenberg H., Bujard H.;

Stunnenberg H., Bujard H.;

Phylymorphism of the precursor for the major surface antigens of plasmodium falciparum merozoites: studies at the genetic level.";

EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Bukaryota; Alveolata; Apicomplexa; Haemospoxida; Plasmodium
NCBI_TaxID=70153;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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J. Mol. Biol. 195:273-287(1987).
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Matches 9; Conserv
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16:1206-1206(1988)

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-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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MEDLINE-88143999; Pubmed=3278296;
Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
"Mexozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";
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SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                              PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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MEDUINE-86205236; PubMed=3517809;
Weber J.L., Leininger W.M., Lyon J.A.;
Wariation in the gene encoding a major merozoite surface antigen the human malaria parasite Plasmodium falciparum.";
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5835;
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4
kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
PTW: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA EDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBFACE ANTIGENS MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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NCBL_TaxID=57270;
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Pfam; PF00008; EGF; 1.
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkmen M., Benedik M.J.;
"DinI inhibits transcription of Serratia marcescens nuclease.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                                                                            InterPro; IPR000561, EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Pyrimidine biosynthesis; third step. SUBUNIT: HOMODIMER (BY SIMILARITY). SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 1.
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                      PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                      5B59CEEFA2F9A026 CRC64;
                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                                                                                                                                                                                (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dihydroorotase (EC 3.5.2.3) (DHOase) (Fragment)
                                                                                                                                                                                              N-LINKED (GLCNAC,
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                                                                                                                                                                                                                                                                                                                                                                            Score 42.5; DE
Pred. No. 13;
4; Mismatches
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                                                                                                                                                                             POTENTIAL
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QFVKSNSKVITGLTE 1040
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                                                                                                                    EMBL; M37213; AAA29611.1; -
                                                                                                                                                               Transmembrane; GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                       Similarity 60.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          1 OYIKANSKFI-GITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                          1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=615;
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ID PYRC_SERMA
AC Q9S3S1;
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CARBOHYD
CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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and for commercial
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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y., Xu Z., Xuang L., Dong W., Yang J.,

Chen Y., Xue Y., Xu. Y., Lin Y., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T. tengcongensis genome.";

"A complete sequence of T. tengcongensis genome.";

-!- FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form a cetyl-CoA with 3-methyl-2-oxobutanoate (2-isopropylmalate).

-!- CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanoate + COA = acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O.
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          is in
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-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE
SYNTHASE FAMILY. LEUA 1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amocation update)
2-isopropylmalate synthase 2 (EC 4.1.3.12) (Alpha-isopropylmalate
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                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%; Score 41; DB 1; Length 204; 46.2%; Pred. No. 2.9;
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 41; DB 1; Length 384; ilarity 54.5%; Pred. No. 5.5; Conservative 4; Mismatches 1; Indels
          as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                            204 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;
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PROSÍTE; PSO0816; AIPM HOMOCIT_SYNTH_2; 1.
PROSÍTE; PSO0816; PAPA HOMOCIT_SYNTHE Z; 1.
SEQUIENCE 384 AA; 42404 MW; 095310F2COE4A4DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                           EMBL, AF175466, AADS0307.1; ALT_INIT.
INCETPO; IPR002195, DibyGrooracase.
PROSITE: PS00482; DIHYDROOROTASE 1; PARTIAL.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
                              modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
institutions as long
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                                                                                                                                                                                                                                                                                                   Pyrimidine biosynthesis; Hydrolase; Zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.2
Matches 6; Conservative
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          non-profit
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LEUA2 OR TTE0472
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Conservative
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les 8; Conserv
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NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
                                                                                                                                                                                                              SEQUENCE
                                           SEQUENCE
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PEF1_LACLC
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Matches
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
Manalysis of nucleotide sequence of the rightmost 43 kbp of
herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
organization between HVS and Epstein-Barr virus.";
Virology 188:296-310(1992).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
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01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-2002 (Rel. 41, Last annotation update)
Probable acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP phosphodiesterase).
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92333688; PubMed=1321287; Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B. Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%; Score 41; DB 1; Length 899; 50.0%; Pred. No. 13; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          899 AA; 103350 MW; F1429B3770A2885E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92230228; PubMed=1314457;
                                                                                                                                                                                                                                                                       63 OR EERF1
Herpesvirus saimiri (strain 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X64346; CAA45686.1; -. EMBL; M86409; AAA46139.1; -. PIR; G36812; G36812.
                                                                                                                                                                                                                                                 Capsid assembly protein 63.
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214 VKAGAKFVGVT 224
                                                                                                                                              STANDARD;
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3 IKANSKFIGIT 13
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10383;
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                                                                                                     NESULT 10
V120 HSVSA
AC Q01055; DT 01-APR-1993
DT 01-APR-1993
DT 01-APR-1993
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P43013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                           STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witterpeck T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).

-!- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).
-!- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)0 = 4'-phosphopantetheine + apo-[acyl-carrier protein].
-!- SIMILARITY: BELONGS TO THE ACPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NCDO 763; MEDLINE=95096044; PubMed=7798200; Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.; Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.; "Biochemical and genetic characterization of PepF, an oligopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                  Chandler M.S., Smith R.A.; "Chandler M.S., Smith R.A.; "Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence."; Gene 169:25-31(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 4.2;
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SEQUENCE 194 AA; 21208 MW; ABAEC9D00829522C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=96186898; PubMed=8635745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U20964; AAC43728.1; -.
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53.3%;
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147 QYMKSILGFIGITDV 161
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PIR; S46746; S46746
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YHJ9 YEAST
ID YHJ9 YEAST
AC P38694;
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METĀL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactis ssp. lactis lin403.";
Genome Res. 11:731-753(2001).
-!- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO ACIDS WITH A RATHER WIDE SPECIFICITY (BY SIMILARITY).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                1. Bacceriol. 179:4164-4171(1997).
-i- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
ACIDS WITH A RATHER WIDE SPECIFCITY.
-i- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                             "Duplication of the pepP gene and shuffling of DNA fragments on the lactose plasmid of Lactococcus lactis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                    54.1%; Score 40; DB 1; Length 601; 46.7%; Pred. No. 13; 1:ve 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
10-UUN-2002 (Rel. 41, Last annotation update)
PEPF OR LL1727.
                                                                                                                                                                                                                                                                                               InterPro; IPR004438; PepF.
InterPro; IPR001567; Peptidase M3.
InterPro; IPR0010167; Peptidase M3.
Pfam; PF0432; Peptidase M3; I.
TIGRFAMS; TIGR00181; PepF; 1.
PROSITE; PS00142; ZINC PROTEASE; PALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 AA
from Lactococcus lactis.";
J. Biol. Chem. 269:32070-32076(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=1L1403;
MEDLINE=21235186; Pubmed=11337471;
                                           STRAIN=NCDO 763; MEDLINE=97352670; PubMed=9209029; Nardi M., Renault P., Monnet V.;
                                                                                                                                                                                                                                                                                                                                                                                                                  394 394 Z
518 518 F
601 AA; 69674 MW;
                                                                                                                                                                                                                                                                  EMBL; Z32522; CAA83534.1; -.
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284 RYIELRKKILGITDL 298
                                                                                                                                                                                                                                                                             EMBL; X99798; CAA68133.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                 SEQUENCE FROM N.A.
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MEDLINE=9478003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman R., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical aldehyde-dehydrogenase like protein in FIL1-VMA10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 265:2077-2082(1994).
-!- SIMILARITY: BELCNGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
(BY SIMILARITY)
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    -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.

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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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                                                                                                                                                                                                                                                                                                                    EMBL; AE006403; AAK05825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69883 MW;
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284 RYIELRKKILGITDL 298
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Matches 7; Conservative
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391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE C 2743 / KID;
MEDLINE-ATCC 2743 / KID;
MEDLINE-88142549; PubMed=3481422;
Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
"The ribosomal protein gene cluster of Mycoplasma capricolum.";
Mol. Gene. Genet. 210:314-312(1987).
-!- FUNCTION: THIS SYMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.
                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
                                                                                                                                                                          DB 1; Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.7%; Score 39; DB 1; Length 213; 72.7%; Pred. No. 7; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYCOPLESMIC.
-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Print, Provide, adenylatekinase; 1.

PRINTS, PRO0094; ADENYLTKNASE.

PRODOM; PD000657; Adenylate kin; 1.

PROSITE; PS00113; ADENYLATE KINASE; 1.

Transferase; Kinase; ATP-binding.

NP BIND 7 15 ATP ATP (BY SIMILARITY).

SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;
                                                                                                                                              54DADDAEB2A16D4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes; Mollicutes; Entomoplasmatales;
SGD; S0001081; YHR039C.
InterPro; IPR02086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_GLU; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
HYPOTHETICAL protein; Oxidoreductase.
ACT_SITE 384 BY SIMILARITY.
ACT_SITE 389 BY SIMILARITY.
SEQUENCE 644 AA; 71320 MW; S4DADDAEB2A16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See h
or send an email to license@isb-sib.ch).
                                                                                                            BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                               54.1%; Score 40;
60.0%; Pred. No.
ive 1; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P27142; 1ZIN.
InterPro; IPR000850; Adenylate kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X06414; CAA29724.1; -. PIR; S02851; KIYMC.
                                                                                                                                                                                                                                                   1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                      38 ÓIIQDNQKLÍGÍTTL 52
                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 YFKTNSKFIEL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YIKANSKFIGI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma capricolum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entomoplasmataceae.
NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                          KAD_MYCCA
     STTXBBBBB
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Search completed: July 22, 2003, 08:06:39 Job time: 2.39504 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 22, 2003, 08:05:43; Search time 0.55306 Seconds (without alignments) 1574.881 Million cell updates/sec

US-09-806-703A-14 112 1 FNNFTVSFWLRVPKVSASHLE 21

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | 958 clostridium |           |           | 45 clostridium |        |           |           |           |            | 11 impatiens n | tomato | tomato | clostri |        | 21 clostridium | 71 clostridium |            | 56 clostridium | 32 rhizobium m | 55 rhodobacter | 53 escherichia | 44 barley yell | 33 streptomyce | 76 saccharomyc | 36 schizosacch | 56 homo sapien | Ċ          | 30 mus musculu | 29 homo sapien | N     | 56 saccharomyc | _          | 23 salmonella |
|-----------|-----------------------|-----------------|-----------|-----------|----------------|--------|-----------|-----------|-----------|------------|----------------|--------|--------|---------|--------|----------------|----------------|------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|------------|----------------|----------------|-------|----------------|------------|---------------|
|           | 980                   | P049            | P30996    | 060393    | P10845         | P10844 | 710       | 200496    | 309       | 045894     | 001811         | P26002 | P26003 | P46081  | P18640 | P19321         | P23671         | P46082     | 998900         | P72302         | P17055         | 762            | P2904          | P45503         | P0387          | P8713          | 09by60         | 062240     | P4123          | P4122          | P3824 | 4715           | P77390     | 3792          |
|           | ă                     | ā               | ď         | ŏ         | ď              | ă      | Ö         | ŏ         | ď         | Ò          | ŏ              | Ċ.     | Ď,     | À       | 'n,    | Ď,             | Ċ,             | à          | ŏ              | ሷ              | Ď,             | À              | À              | Ã              | ሷ              | ፩              | ö              | ŏ          | ď,             | ď,             | 'n,   | P4.            | Ď,         | Ď,            |
| SUMMARIES | ΙD                    | TETX CLOTE      | BXF_CLOBO | BXG_CLOBO | BXA1 CLOBO     |        | VP2_AHSV6 | BXE_CLOBO | BXE_CLOBU | BXA2_CLOBO | NNSS_INSVN     |        |        |         |        | BXD_CLOBO      | AMY_CLOAB      | BXEN CLOBO | BXEN_CLOBU     | CGMA_RHIME     | CRIA_RHOCA     | YOBD_ECOLI     | RRPO_BYDV1     | FTSQ_STRGR     | AI2M YEAST     | YDMS_SCHPO     | SMCY HUMAN     | SMCY_MOUSE | SMCX_MOUSE     | SMCX_HUMAN     |       | YJ89 YEAST     | CITC_ECOLI | FIMC_SALTY    |
|           | DB                    | н               | Н         | H         | Н              | н      |           | Н         | -         | -          | Н              | 1      | -      | -       | Н      | -              | -              | -          | Н              | -              | Н              | -              | Ä              | ٦              | -              | ٦              | Н              | 7          | ч              | Н              | Н     | Н              | Н          | 7             |
|           | Query<br>Match Length | 1314            | 1274      | 1296      | 1295           | 1290   | 1021      | 1250      | 1250      | 1295       | 449            | 464    | 467    | 1196    | 1290   | 1276           | 760            | 1162       | 1162           | 639            | 241            | 152            | 867            | 208            | 789            | 1337           | 1539           | 1548       | 1554           | 26             | 237   | 728            | 352        | 230           |
| df        | Ouery<br>Match        |                 | 54.5      | 4.        | ά.             | ä      | ö         | 50.0      | ò         | 20.0       | 46.4           | 46.4   | 46.4   | 45.5    | 42.9   | 42.4           | 42.0           | 41.1       | ٠              |                |                | 38.4           | œ              | ζ.             | 7              | 7              |                | 7          | 37.5           | 7              | 7     | ۲.             | 36.6       | 36.2          |
|           | Score                 | 112             | 61        | 61        | 59             | 28     | 57        | 26        | 26        | 26         | 52             | 52     | 25     | 51      | 48     | 47.5           | 47             |            | 46             | 45             | 44             |                |                |                |                |                |                | 42         | 42             | 42             | ٠     | 41.5           | 41         | 40.5          |
|           | Result<br>No.         | 1               | 7         | m         | 4              | Ŋ      | 9         | 7         | 80        | σ          | 10             | 11     | 12     | 13      | 14     | 15             |                | 17         | 18             | 19             | 20             | 21             | .22            | 23             | 24             | 25             | 56             | 27         | 28             | 29             | 30    | 31             | 32         | 33            |

| 36 schizosacch | .7 paralichthy | 6 saccharomyc | 6 mycoplasma | 6 schizosacch | 2 drosophila | 14 salmonella | 19 saccharomyc | 9 methanopyru | 10 influenza a |            |            |
|----------------|----------------|---------------|--------------|---------------|--------------|---------------|----------------|---------------|----------------|------------|------------|
| 87600          | . P9281        | Q0427         | P4770        | 074456        | P5895        | P3760         | P4704          | Q8tw2         | P0347          | P0346      | P06819     |
| YA98 SCHPO     | NU3M PAROL     | YMX2 YEAST    | PARA MYCGE   | PEF1 SCHPO    | G22C_DROME   | DACD_SALTY    | YJE8 YEAST     | LE22 METKA    | NRAM IAWIL     | NRAM IAPUE | NRAM_IAPAR |
| 7              | н              | Н,            | н            | -             | н            | -             | -              | н             | н              |            |            |
| 535            | 116            | 118           | 569          | 288           | 383          | 390           | 396            | 402           | 453            | 454        | 469        |
| 36.2           | 35.7           | 35.7          | 35.7         | 35.7          | 35.7         | 35.7          | 35.7           | 35.7          | 35.7           | 35.7       | 35.7       |
| 40.5           | 40             | 40            | 40           | 40            | 40           | 40            | 40             | 40            | 40             | 40         | 40         |
|                |                |               |              |               |              |               |                |               |                |            |            |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                           NAT. Struct. Biol. 4:788-792(1997).
-1- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PREIPHERAL NEURONAL SYRAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPERIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN- |- PHE-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCRAINS L AND H. THESE REMAIN LINKED BY A. DISULFIDE BRIDGE AND AND ATTER SEPARATION.
MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PR0010163; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
                                                                                                                                                                                                                        Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
                                                    MEDLINE-93063293; PubMed=1331807; Schiato G., de Laureto P.P., Schiatov G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.; "Tetanus and botulinum-B neurotoxins block neurotransmitter release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN- |-PHE-77 BOND IN
                                                                                                                                                                                                                                                            "Structure of the receptor binding fragment HC of tetanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150550 MW; 134C3657133EF81D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETANUS TOXIN LIGHT CHAIN.
TETANUS TOXIN HEAVY CHAIN.
ZINC (CATALYTIC) (BY SIMIL
                                                                                                                                                                                     874-1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                             by proteolytic cleavage of synaptobrevin.";
Nature 359:832-835(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY ZINC (CATALYT
                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF MEDLINE=97475217; PubMed=9334741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X04436; CAA28033.1; -. EMBL; M12739; AAA23282.1; -. EMBL; X06214; CAA29564.1; -.
                                    IDENTIFICATION OF SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                 BOND OF SYNAPTOBREVIN-2
EMBO J. 11:3577-3583 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GANGLIOSIDE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1AF9; 29-APR-98.
PDB; 1A8D; 14-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, A25689; BICLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNAPTOBREVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; M27.001;
                                                                                                                                                                                                                                                                                neurotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT MET
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                             Sax M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F., Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; Cleavage of tembers of the synaptobrevin/vamp family by types D and E botulinal neurotoxins and tetanus toxin.";
J. Biol. Chem. 269:12764-12772(1994).
-!-FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPRETIDASE THAT CAPALZES THE HYDROLYSIS OF THE 58-GLN-|-LYS-59 BOND OF SYNAPTOBREVINS-1 AND -2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94013372; PubMed=8408542; Cangapel K. Callins M.D.; Campbell K., Callins M.D.; Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Secreted.
-:- MISCELLANBOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2?.
                                                                                                                                                                                                                                                                                               Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberts T.A., Thompson D.E., "Sequence of the gene encoding type F neurotoxin of Clostridium botulinum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93012902; PubMed=1398040;
East A.K., Richardson P.T., Allaway D., Collins M.D.,
Roberts T.A., Thompson D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORMATION AND TOXIN BINDING, RESPECTIVELY
                                                                                                                                1274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEMS Microbiol. Lett. 75:225-230(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Microbiol. 31:2255-2262(1993)
946 FNNFTVSFWLRVPKVSASHLE 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94230352; PubMed=8175689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curr. Microbiol. 29:69-77(1994)
                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 634-1002 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION OF SUBSTRATE
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                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             East A.K., Collins M.D.;
                                                                                                                                                                       01-JUL-1993 (Rel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 23387;
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1491;
                                                                                                                                                                                                                                                        (Bontoxilysin F)
                                                                                                                                                                                                                                                                                                                                             Clostridium.
                                                                                                                                CLOBO
                                                                                       RESULT 2
BXF_CLOBO
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21; Conservative

Matches

Local Similarity

Query Match

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Gaps

ó;

Indels

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0; Mismatches

Length 1314;

100.0%; Score 112; DB 1; 100.0%; Pred. No. 1.8e-10;

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CLOBO
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METĀL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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BXA1 CLOBO
        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use 'by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CA
                                                                                                                                                                                                                                                                                                                                            Transmembrane, Hydrolase, Metalloprotease, Zinc.
1 436
437 1274 BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.
227 ZINC (CATALYTIC) (BY SIMILARITY).
228 228 BY SIMILARITY.
231 ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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INTERCHAIN (PROBABLE).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BoNT/G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 1; Length 1274;
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146709 MW; 5B99756A7438B921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                              MEROPS; M27.002; -.
InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; BONTOXILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; I.
Neurotoxin; Transmembrane; Hydrolase; CHAIN
                                                                                                EMBL, M92906, AAA23263.1, -. EMBL, S73676, AAC60475.1; -. EMBL, X70820, CAA50151.1, -. EMBL, X70816, CAA50147.1; -. HSSP, P10845; 3BTA.
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930 YQNFSISFWVRIPK 943
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ACT SITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P10845; P18639; P01561; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A, heavy-chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOTULINUM NEUROTOXIN G, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN G, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 MEROYS; M27.002; -...
InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Neurotoxin; Hydrolase; Metalloprotease; Zinc.
INIT MET 0 BY SIMILARITY.
CHAIN
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Pred. No. 0.049;
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                                                                                                                                                                                                                                            entities requires a license agreement (St or send an email to license@isb-sib.ch).
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MEDLINE=90235864; PubMed=2185020;
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                                                                                                                                                                                                                                                                                                                                  EMBL; X74162; CAA52275.1; -. HSSP; P10845; 3BTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.5%;
38.1%;
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Clostridium botulinum.
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Best Local Similarity
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Dasgupta B.R., Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
                                                                                                                                                                                                                                                                 MEDLINE=96096783; PubMed=8521962; Publita R., Kumon H., Oguma K.; Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.; "Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins."; FEBS Lett. 376:41-44(1995).
                                                                                                                                                                      Betley M.J., Somers E., Dasgupta B.R.; "Characterization of botulinum type A neurotoxin gene: delineation of the N-terminal encoding region.";
                                    East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION OF SUBSTRATE.
MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.
Jahn R., Niemann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85285016; PubMed=3896784; Shone C.C., Hambleton P., Melling J.; Inactivation of Clostridium botulinum type A neurotoxin by trypsin Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94063091; PubMed=8243676; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Betulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds "; FEBS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Niece R.L.;
the heavy chain into two
                                                                                                                                                                                                                                                                                                                                                                         Schmidt J.J., Sartymoorthy V., Dasgupta B.R.; "Partial amino acid sequence of the heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasgupta B.R., Dekleva M.L.;
"Botulinum neuroctoxin type A: sequence of amino acids at the
"Lerminus and around the nicking site.";
Biochimie 72:661-664(1990)
                                                                                                                                                                                                               ochem. Biophys. Res. Commun. 162:1388-1395(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 119:900-904(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 448-464 AND 872-895.
MEDLINE=89024662; PubMed=3178218;
Sathymoorthy V., Dasgupta B.R., Foley J., I
Botulinum neurotoxin type A: cleavage of halves and their partial sequences.,
Arch. Biochem. Biophys. 266:142-151(1988).
            STRAIN=62A;
MEDLINE=97016817; PubMed=8863443;
                                                                                                                                                           WEDLINE=89350959; PubMed=2669749;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84178501; PubMed=6370252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91120847; PubMed=2126206;
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                                                                                                                                                                                                                                                                                                                                                                                                      botulinum neurotoxin type A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-5 AND 444-456
                                                                                                                                  SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                                          SEQUENCE OF 1-18 FROM N.A.
 SEQUENCE OF 1-65 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 448-482
                                                                                                                                                                                                                                                      STRAIN=Type A NIH;
                                                                                                                                                                                                                                                                                                                                                  OF 1-16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for toxicity.";
Nat. Struct. Biol. 5:898-902(1998).

-- FUNCTION: Inhibite acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the call surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALITIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates
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Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and
                                                                                                                                            MEDLINE=21556941; PubMed=11700044;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
Siste-directed mutagenesis identifies active-site residues of the
light chain of botulinum neurotoxin type a.";
Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
"Proteolysis of SNAP-25 by types E and A botulinal neurotoxins."; J. Biol. Chem. 269:1617-1620(1994).
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Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXIEVSIN. 1.
Prodom; PD001963; BONTOXIJYSin; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
                                                                                                               GLU-261; PHE-265 AND TYR-365
                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
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-!- SUBCELLULAR LOCATION: Secreted.
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PIR; S09492; S09492.
PDB; 3BTA; 01-OCT-99.
MEROPS; M27.002; -.
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Biochimie 70:811-817(1988).
                            STRAIN=OKRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
ACT_SITE
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   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94013372; PubMed=8408542; Campbell K., East A.K., Collins M.D.; "Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92384550; PubMed=1514783;
Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
Minton N.P.,
                                                                                                               F->A: DECREASE IN ENZYMATIC ACTIVITY Y->A: DECREASE IN ENZYMATIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
   LIGHT-CHAIN
           HEAVY-CHAIN
                                                                                               DRASTIC DECREASE IN ENZYMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dasgupta B.R., Datta A.;
"Botulinum neurotoxin type B (strain 657): partial sequence and
similarity with tetanus toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of the Clostridium botulinum structural gene
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the type B neurotoxin and determination of its entire nucleotide sequence.";
                                                                                                                                                                                                                                                                                BXB_CLOBO STANDARD; PRT; 1290 AA. P1084; P1084; P10843; P101-1999 (Rel. 1, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Botulinum neurocoxin type B precursor (EC 3.4.24.69) (BONT/B)
                                                                                                                                                                                    52.7%; Score 59; DB 1; Length 1295; 57.1%; Pred. No. 0.11;
                                                                                                                                                                                                      2; Indels
                                                                                                                                                          S -> K (IN REF. 8).
MW; 858342F754862579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
  BOTULINUM NEUROTOXIN A, BOTULINUM NEUROTOXIN A,
                                                                                                                        Y->A: DECREASE IN ENZ
P -> Q (IN REF. 1).
Z -> P (IN REF. 9).
T -> L (IN REF. 8).
S -> K (IN REF. 8).
                   (CATALYTIC)
                                    (CATALYTIC)
(CATALYTIC)
                                                                                                                                                                                             Pred. No. 0.11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appl. Environ. Microbiol. 58:2345-2354(1992)
                                                     INTERCHAIN
                                                                              POTENTIAL.
                                                                      POTENTIAL
                                                                                                      ACTIVITY
                                                                                        V -> A.
                   ZINC
                                   ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89000987; PubMed=3139097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 633-993 FROM N.A. STRAIN=NCTC 7273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-44 AND 441-466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 35-245 FROM N.A. STRAIN=NCTC 7273;
                                                                                                                                                                   149322
                                                                                                                                                                                                                               1 FUNFTVSFWLRVPK 14
                                                                                                                                                                                                      Conservative
                                                                                                                                        479
                                                                      646
675
26
261
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                                                                                                                                                          891
                                                                                                                                                          891 89
1295 AA;
                                                                                                                                                                                           Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                     (Bontoxilysin B)
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1491;
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365
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CHAIN
CHAIN
METAL
ACT SITE
METAL
                                                                                                                        MUTAGEN
                                                                                                                                                         CONFLICT
                                                     DISULFID
                                                                                                                                                                                    Query Match
                                                            DISULFID
                                                                      TRANSMEM
                                                                              FRANSMEM
                                                                                                                                         CONFLICT
                                                                                              MUTAGEN
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                                                                                    VARIANT
                                             METAL
                                                                                                                                                                                                    Matches
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by protecolytic cleavage of synaptobrevin.",

Nature 359:832-835(1992)

Nature 359:832-835(1992)

PUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHEAL NEURONAL SYNAPEGS, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN WOVE BETWANDER TO AND PRESYNAPIT C NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPERIDASE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF

SYNAPTOBREVIN-2.

C.-!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the

neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No

detected action on small molecule substrates.

C.-!- SUBUMIT: DISULETUB-LIMIKED HETERODIMER OF A LIGHT CHAIN (L) AND A

HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,

WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no new modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=93064694; PubMed=1429690;
Schlavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;
"Botulinum neurotoxins are zinc proteins.";
J. Biol. Chem. 267:23479-23483(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93063293; PubMed=1331807; Schiadro G., de Laureto P.P., Schiadro G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucio C.; and "Tetanus and botulinum-B neurotoxins block neurotransmitter release
                                                                                                                  schmidt J.J., Sathyamoorthy V., Dasgupta B.R.; Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANBOUS: THERE ARE SEVEN ANTICENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, F, AND G.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Metalloprotease; Zinc.
                                                                                                                                                                                                                                Arch. Biochem. Biophys. 238:544-548(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frodom; Prod1963; BONTOXILYSIN.
PROSITE; PS001963; BONCOXILYSIN; I.
Neurotoxin; Transmembrane; Hydrolaser INIT MET

CHAIN
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Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
                                                           MEDLINE=85197963; PubMed=3888113;
Schmidt J.J., Sathvamoorthv V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR000395; Bontoxilysin.
                                                                                                                                                                                                                                                                                                           IDENTIFICATION AS ZINC-PROTEASE
SEQUENCE OF 1-16 AND 441-458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M81186; AAA23211.1; -. EMBL; Z11934; CAA77991.1; -. EMBL; X70817; CAA50148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION OF SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440
1290
229
230
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PIR; S07155; S07155.
PIR; S08562; S08562.
PIR; S08573; S08573.
PIR; A48940; A48940.
HSSP; P10845; A48940.
HSSP; M27.002; F1.
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neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
                      Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 419-426.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                         FROM N.A.
                                                       NCBI_TaxID=1491;
                                                                                        STRAIN=Beluga
                                             Clostridium
                                                                           SEOUENCE
                                                                                                                                                                                                                                gene.
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
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                                                                                                                                                                                                                                                                                African horse sickness virus 6 (AHSV-6) (African horse sickness virus
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                MEDLINE-9827831; PubMed=9617769;
Milliams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Milliams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Milliams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Milliams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
Morse sickness virus serotype 6: evolutionary relationships within and between the orbivinuses.";
Wirus Res. 53:53-73(1998)
-!- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
MAJOR TARGET OF THE HOST IMMUNGENIC RESPONSE.
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
                                                                                                           ö
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 ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.9%; Score 57; DB 1; Length 1051; 47.6%; Pred. No. 0.18;
                                                                                    Score 58; DB 1; Length 1290; Pred. No. 0.15;
                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                               D21746E2C024DF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1051 AA; 122326 MW; 2B04DB9E389F4B5F CRC64;
                      T -> M (IN REF. 4).
R -> G (IN REF. 2).
A -> S (IN REF. 2).
S -> R (IN REF. 4).
             INTERCHAIN (PROBABLE)
                                                                                                                                                                                                                                                                                           (serotype 6)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
NCBI _TaxID=86060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                           (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                        PRT; 1051 AA.
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                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VP2.
                                                                150670
                                                                                     51.8%;
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                                                                                                 64.38;
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922 FLDFSVSFWIRIPK 935
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Pfam; PF00898; Orbi VP2; 1.
                                                                                                                              1 FNNFTVSFWLRVPK 14
                                                                                                                                                                                                                                                          Outer capsid protein VP2.
S2 OR L2.
                                                                                              Local Similarity 64.3
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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                                                                                                                                                                                                        STANDARD;
           445
29
217
224
                                                     463
                                                     463 46
1290 AA;
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SEQUENCE 10
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01-JUL-1993
15-JUN-2002
                                                                                                                                                                                                                071024;
15-DEC-1998
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15-DEC-1998
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Q00496;
                                                                                                                                                                                                        VP2 AHSV6
                                         CONFLICT
CONFLICT
SEQUENCE
           DISULFID
CONFLICT
CONFLICT
                                                                                     Query Match
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J. Biol. Chem. 269:1617-1620(1994).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-|-ILE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92174922; PubMed=1S41280; Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.; Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.; "The complete amino acid sequence of the Clostridium borulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 BOND IN SNAP-25.

CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBMUT: DISULFIDE LINKED HETEROLIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94124495; PubMed=8294407; Binz T., Blanz T., Blanz T., Suedhof T.C., Jahn R., Niemann H.; Maraeaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H.; Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.; "The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins."; J. Biol. Chem. 265:9153-9158(1990).
                                                                                                                                                                                                                                                                                                                                  Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Bentenati F., Wilson B.C., Montecucco C.; Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds "; FEBS Lett. 335:99-103(1993).
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MEDLINE=85197963; PubMed=3888113;
Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gimenez J.A., Dasgupta B.R.; "Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the site trypsin nicks and homology with tetanus
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 183:107-113(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 204:657-667(1992)
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MEDLINE=90264400; PubMed=2160960;
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                                                                                                                                                                                                                                                                                                    MEDLINE=92181428; PubMed=1543481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochimie 72:213-217(1990).
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STRAIN=BL6340;
                                                                                                                                                                  STRAIN=5262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
         SUBCELLULAR LOCATION: Secreted.

MISCELLANBOUS: THERE ARE SEVEN ANTICENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A. B, Cl, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                               BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTY.
ZINC (CATALYTY.
ZINC (CATALYTY.)
INTERCHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Bontoxilysin E).
Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
                                                                                                                                                                                                                                               InterPro; IPR0001395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1250; 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143712 MW; D9FCE26DDA041EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           R -> G (IN REF. 2).

C -> S (IN REF. 2 AND 3).

R -> A (IN REF. 2).

I -> L (IN REF. 2).

FE -> LQ (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                             -> A (IN REF. 2).
 PORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 43181, and ATCC 43755; MEDLINE=92181428; PubMed=1543481;
                                                                                                                                           EMBL; X62089; CAA43999.1; -. EMBL; X62683; CAA44558.1; -.
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911 YKNFSISFWVRIP 923
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                             PIR; A60027; A60027.
PIR; B35294; B35294.
PIR; JH0257; JH0257.
PIR; S08575; S08575.
PIR; S18111; S18111.
PIR; S21178; S21178.
HSSP; P10845; 33FTA.
MEROPS; M27.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              966 96
1194 119
1250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium.
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gimenez J., Foley J., Dasgupta B.R.;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
FASEB J. 2:41750-41750 (1988)
-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYMAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYMAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91237316; PubMed=2033376;
Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K.,
Yokosawa N., Yashiki T., Oguma K.;
"Cloning of a DNA fragment encoding the 5'-terminus of the botulinum
type E toxin gene from Clostridium butyricum strain BL6340.";
J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755)."; Ejochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
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ZINC (CATALYIIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
K -> M (IN REF. 2).
MW, 8171B5B2C2312857 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
INIT MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1250;
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or send an email to license@isb-sib.ch).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn WTpeptdse.
Pfan; PP01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X62088; CAA43998.1; -. EMBL; X53180; CAA37321.1; -.
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                                                                                                                                                                 SEQUENCE OF 1-251 FROM N.A.
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PIR, S16145, S16145.
HSSP, P10845; 3BTA.
MEROPS; M27.002; -.
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212 21
215 21
411 42
229 22
1250 AA;
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Best Local Similarity
Matches 7; Conserv
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R Probom, PRO130130; Zn.MPpeptdse.
R Probom, PRO142; Peptidase M37; 1.
R Probom, PRO142; Peptidase M37; 1.
R Probom, PRO142; Peptidase M37; 1.
R PROSTTE, PSO0142; ZINC_PROTEASE; FALSE_NEG.
W Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
T INIT_MET 0 0 BY SIMILARITY.
T CHAIN 148 1295 BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
T METAL 222 ZZINC (CATALYTIC) (BY SIMILARITY).
T METAL 222 ZZINC (CATALYTIC) (BY SIMILARITY).
T METAL 226 ZZ ZINC (CATALYTIC) (BY SIMILARITY).
T DISULID 499 453 INTERCHAIN (BY SIMILARITY).
T DISULED 1234 1279 BY SIMILARITY.
T TRANSMEM 626 646 POTENTIAL.
InterPro; IPR000395; Bontoxilysin.
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1295
222
222
226
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1279
646
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626 64
655 67
1295 AA;
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Q01811;
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Rast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium toxin components in proteolytic Clostridium toxin botulinum types A, B, and F: evidence of chimeric sequences in the T. Syst. Bacteriol. 46:1105-112(1996).

In J. Syst. Bacteriol. 46:1105-112(1996).

In FUNCTION: Inhibits acceylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor—mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-[-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acceptochine release results in flacid paralysis, with frequent heart or respiratory failure (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroexecytosis apparatus, synaptobrevins, FNAP25 or syntaxin. No detected action on small molecule substrates.
SUBNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity).
SUBCELUIAR LOCATION: Secreted.
MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                     BXA2_CLOBO STANDARD; PRT; 1295 AA.
454894; P77780;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNI/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A, heavy-chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Kyoto-F;
MEDLINE=94143603; PubMed=8110180;
Willems A., East A.K., Lawson P.A., Collins M.D.;
Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison with other clostridial neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. Microbiol. 144:547-556(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97016817; PubMed=8863443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X73423; CAA51824.1; -. EMBL; X87974; CAA61234.1; -. HSSP; P10845; 3BTA. MEROPS; M27.002; -.
                                                 911 YKNFSISFWVRIP 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-65 FROM N.A.
                      1 FNNFTVSFWLRVP 13
                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                BOTA OR BNA OR ATX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium.
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                                                                                                                                                                 BXA2_CLOBO
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                                                                                                          Gaps
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NCBI_TaxID=31622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92331780; PubMed-1385787; de Haan P., de Avila A.C., Kormelink R., Westerbroek A., de Haan P., the Avila A.C., Kormelink R., desterbroek A., follopach R.; Gielen U.J., Peters D., Goldbach R.; The nucleotide sequence of the S RNA of Impatiens necrotic spot virus, a novel tospovirus.";
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                                                  Score 56; DB 1; Length 1295;
Pred. No. 0.33;
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                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
SDA04A13D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51197 MW; C46AC1372B114CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Impatiens necrotic spot virus (strain NL-07) (INSV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION; FORMS FILAMENTOUS INCLUSION BODIES.
                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Nonstructural protein NS-S.
                                                                                                                                                                                                                                                                                                                                                         449 AA
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                                                                                                          5; Mismatches
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  149279
                                                     50.0%;
                                                                                                                                                                                              : ||: |||:::||
937 YENFSTSFWIKIPK 950
                                                                                                                                                               1 FNNFTVSFWLRVPK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus, a novel tospovirus.
FEBS Lett. 306:27-32(1992)
                            Query Match
Best Local Similarity 50.v.
7; Conservative
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Best Local Similarity 45.0
Matches 9; Conservative
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1491;
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BXC1_CLOBO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV). Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.VCBI_TaxID=36413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomato spotted wilt virus (strain Bulgarian L3) (TSWV).
Viruses, ssRNA negative-strand viruses, Bunyaviridae, Tospovirus.
VCBI_TaxID=36415;
                                                                                                                                                                                MEDLINE=90264829; PubMed=1693160;
de Haan P., Wagemakers L., Peters D., Goldbach R.;
"The S RNA segment of tomato spotted wilt virus has an ambisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINES-9113-150; PubMed=1993884;
MAISS E., Ivanova L., Breyel E., Adam G.;
"Cloning and sequencing of the S RNA from a Bulgarian isolate of tomato spotted wilt virus.";
J. Gen. Virol. 72:461-464(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JQ0547; MAVUWC.
InterPro; IPR004915; Bunya NS-S_2.
Pfam; PF03211; Bunya NS-S_2; 1.
Nonstructural protein.
SEQUENCE 464 AA; 52448 MW; AE5519179F9EF377 CRC64;
                                                                                                                                                                                                                                  J. Gen. Viról. 71:1001-1007(1990).
                                               01-MAY-1992 (Rel. 22, Created)
01-WAY-1992 (Rel. 22, Last sequence update)
01-UN-1994 (Rel. 29, Last annotation update)
Nonstructural protein NS-S.
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01-MAY-1992 (Rel. 22, Laat sequence update)
01-UIN-1994 (Rel. 29, Last amotation update)
Nonstructural protein NS-S.
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239 SHFKLSLWLRVPKV 252
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                       STANDARD;
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ID VNSS_TSWVL
AC P26003;
                      TSW1
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MEDLINE=2231894; PubMed=1567404;
Tsuzuki K., Kimura K., Fujii, N., Yokosawa N., Oguma K.;
"The complete nucleotide sequence of the gene coding for the nontoxic-nonhemagglutinin component of Clostridium botulinum type C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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80.0%; Pred. No. 2.1;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                     Score 52; DB 1; Length 467;
Pred. No. 0.51;
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                                                  InterPro; IPR004915; Bunya NS-S_2.
Pfam, PF03231; Bunya NS-S_2; 1:
Nonstructural protein.
SEQUENCE 467 AA; 52413 MW; 38ESCA4E802DB6DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Botulinum neurotoxin type Cl, nontoxic component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p18640;
01-NOV-1990 (Rel. 16, Created)
10-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
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EMBL; D13926; BAA03024.1; -. PIR; JQ0954; MNVUW1.
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243 SHFKLSLWLRVPKV 256
                                                                                                                                                                                                                                                                                                                    2 NNFTVSFWLRVPKV 15
                                                                                                                                                                    Query Match
Best Local Similarity 64.3.
Pest Local Similarity 64.3.
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nes 8; Conservative
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STRAIN=D-SA, and D-1873;
MEDLINE=89339741; PubMed=2668193;
MOTLISH: K., Syuto B., Kubo S., Oguma K.;
Motlecular diversity of neurotoxins from Clostridium botulinum type D
                                                                                                                                                                                                                                                                                                                                                                                                       BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INFERCHAIN (PROBABLE).
P -> T (IN REF 2).
MW; 71FBE379F97129E8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BONT/D)
                                                                                                                                                                                                                                               PRINTS, PRO0760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC PROFEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc. INIT MET 0 0 0 CHAIN
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6; Mismatches
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Nucleic Acids Res. 18:5556-5556(1990).
                                                                                                                                                                                                  Zn_MTpeptdse.
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                                                                                                                                                           InterPro; IPR000395; Bontoxilysin
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                                                                                                                                                                                                                            Pfam; PF01742; Peptidase M27; 1.
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934 YESFSISFWIRINK 947
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1290
228
229
232
452
                                                                                                                                                                                               InterPro; IPR000130;
   PIR; S11291; S11291.
PIR; A35396; A35396.
PIR; A43503; A43503.
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                                                                                             HSSP; P10845; 3BTA.
MEROPS; M27.002; -.
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P19321;
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Matches
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- I- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.

- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
detected action on small molecule substrates.

- SUBBUIT: DISCUILIDE-LIMED HETERODIMER OF A LIGHT CHAIN (L) AND A
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Establishment of a monoclonal antibody recognizing an antigenic site common to Clostridium botulinum type B, C1, D, and E toxins and
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90370487; PubMed=2204031;
Hauser D., Eklund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
Baguet P., Popoff M.R.;
"Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
Nucleot Acids Res. 18:4924-4924(1990).
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SEQUENCE FROM N.A.

MEDLINE=91024999, PubMed=2222445;

Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,

Yokosawa N., Takeshi K., Syuto B., Oguma K.;

The complete nucleotide sequence of the gene coding for botulinum type CI toxin in the C-ST phage genome.",

Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
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MISCELLANBOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
BOTULINUM NEUROTOXIN: TYPES A, B, Cl, D, E, FAND G,
MISCELLANBOUS: BOTULINUM TYPE CI NEUROTOXIN IS SYNTHESIZED BY CSTRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
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MEDLINE=88153072; PubMed=2450068;
Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Pujii N., Kimura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94038966; PubMed-7901002;
Blasi J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
"Botulinum neurotoxin Cl blocks neurotransmitter release by means o
                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
   precursor (EC 3.4.24.69) (BoNT/C1)
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Botulinum neurotoxin type
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                                                                    Clostridium botulinum.
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"Establishment of
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                                      (Bontoxilysin C1)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F., Roques B., Fykse B.M., Suedhof T.C., Jahn R., Niemann H.; Roques B., Fykse B.M., Suedhof T.C., Jahn R., Niemann H.; Cleavage of members of the synaptobrevin/VAMP family by types D and F botulinal neurotoxins and tetanus toxin. "J. Biol. Chem. 269:12764-12772(1994).

-I. FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERRIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDORPEPTIBAL CLEAVES THE 60-LYS-|-LEU-61 BOND OF
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REOPS; M27.002; ...

RILGEPTO; IPR000395; Bontoxilyain.

BRINTS; PR00706; Sun'Tipeptdse.

BRINTS; PR00706; BONTOXILYSIN.

BRINTS; PR00706; BONTOXILYSIN.

BROSITE; PR00142; ZINC_PROTEASE; 1.

BROSITE; PR00142; ZINC_PROTEASE; 1.

BROSITE; PR00142; ZINC_PROTEASE; 1.

FT CHAIN 1 442 BOTULINUM NEUROTOXIN D, HIGHT-CHAIN.

FT CHAIN 443 1276 BOTULINUM NEUROTOXIN D, HEAVY-CHAIN.

FT CHAIN 229 229 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 230 BY SIMILARITY.

FT ACT_SITE 230 230 BY SIMILARITY.

FT ACT_SITE 230 233 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 230 SINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                SYNAPTOBREVING.

CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL PRORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANBOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G. MISCELLANBOUS: BOTULINUM TYPE D NEUROTOXIN IS SYNTHESIZED BY D STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
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42.4%; Score 47.5; DB 1; Length 1276;
Best Local Similarity 40.9%; Pred. No. 8.3;
Matches 9; Conservative 7; Mismatches 5; Indels 1,
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ND -> LQ (IN STRAIN D-1873).

R -> T (IN STRAIN D-SA).

R -> F (IN STRAIN D-1873).

A -> D (IN STRAIN D-1873).

A -> D (IN STRAIN D-1873).

N -> K (IN STRAIN CB16).

N -> K (IN STRAIN CB16).
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457 R -> T (IN STRAIN D-SA)
462 A -> D (IN STRAIN D-187
489 K -> N (IN STRAIN CB16)
644 N -> K (IN STRAIN CB16)
1122 Q -> R (IN STRAIN CB16)
1122 Q -> R (IN STRAIN CB16)
1146871 MW; C1ECSOF46C8233E2 CR
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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MEDLINE=94230352; PubMed=8175689;
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EMBL, S49407; AAB24244.1; -.
PIR, S11455; A11455.
HSSP; P10845; 38TA.
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037369 tomato spot

088900 tospovirus.

091brz clostridium

053550 clostridium

045916 clostridium

045916 clostridium

092x77 clostridium

091x85 caenorhabdi

09m1n3 arabidopsis

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091brz clostridium

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"Fragment C of Tetarus Toxin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, PATIS4828; AAF73267.1; -.
HSSP; P04958; 1A8D.
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAWMA; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tetanus toxin (Fragment).
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Pred. No. 1.7e-10;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 FNNFTVSFWLRVPKVSASHLE 21
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Maximum DB seq length: 200000000
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HSSP; P10845; 3BTA.
MEROPS; M27.002; -.
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                                                            057236; 045863
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MEDLLINE=92352228; PubMed=8486245;
Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.
Richardson P.T.;
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                                           Clostridium tetani.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                               Length 1310;
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                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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InterPro; IPR00130; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1268 AA; 145513 MW; 963040091AC15ED2 CRC64;
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                                                                                                                                                                                                                                                                                                                                1310 AA; 150316 MW; 9EADDC914418E450 CRC64;
                                                                                                                                   Shumin Z., Dianliang L.; "Cloning and sequence analysis of tetanus toxin gene."; "Cloning and sequence analysis of tetanus toxin gene."; Submitted (UN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF389424; AAK72964.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                           InterPro; IPR000395; Bontoxilysin.
InterPro; IPR001064; Crystallin.
InterPro; IPR001030; Zn WTpeptdse.
Pram; PF01742; Peptidase_M27; 1.
ProDow; PD001963; Bontoxilysin; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 112; DB 2; 100.0%; Pred. No. 5.2e-10;
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Q45851;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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922 YQNFSVSFWVRIPK 935
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                              Tetanus toxin (Fragment).
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nes 9; Conservative
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Clostridium baratii.
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=1513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LANGELAND;
MEDLINE=S8404102; PubMed=9732534;
MEDLINE=8404102; M. Hidlm S., Collins M.D.;
East A.K., Bhandari M., Hidlm S., Collins M.D.;
Hanalysis of the botulinum neurotoxin type F gene clusters in proteclytic and nonproteclytic Clostridium botulinum and Clostridium
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Pred. No. 0.19;
5; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=NCTC 10281;
Hutson R.A., Collins M.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
BONT/B.
                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Botulinum neurotoxin type F (BONT/F protein).
1278 AA.
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InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Bontoxilysin, 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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EMBL; X81714; CAA57358.1; -.
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EMBL, X70821; CAAS0152.1; -.
EMBL; X99064; CAA67512.1; -.
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931 YQNFSISFWVRIPK 944
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Matches 8; Conservative
PRELIMINARY;
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                                                                                                                                                                                         Clostridium botulinum.
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ID Q4
AC Q4
DT 01
DT 01
DE B0
GN B0
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Kirma N., Ferreira J.L., Baumstark B.R.; "Characterization of six type A strains of Clostridium botulinum that
                                                                                                                                                                                                   Lalli G., Herreros J., Osborne S.L., Montecucco C., Rossetto O., Schiavo G., "Functional characterisation of tetanus and botulinum neurotoxins
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                              Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 58; DB 2; Length 441; 64.3%; Pred. No. 0.2;
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InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Pptidase M27; 1.
ProDom; P0001953; Bontoxilysin; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1291 AA; 150824 MW; D7CA07BAE2EBBCD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 441
52772 MW; 721D0B468E8C95A4 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                               MEDLINE=99343691; PubMed=10413679;
                                                                                                                                                                                                                                                                            binding domains.";
J. Cell Sci. 112:2715-2724 (1999).
EMBL; AJZ4228; CAB43706.1; --
HSSP; P10845; 3BTA.
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64.3%;
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923 FLDFSVSFWIRIPK 936
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81 FLDFSVSFWIRIPK 94
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Matches 9; Conserv
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                                                                                                       NCBI_TaxID=1491;
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01-MAR-2002
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Q93G71
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                                                                                                                                                                       MEDLINE=94013372; PubMed=8408542; Caplins M.D.; Campbell K., East A.K., Collins M.D.; Campbell K., East A.K., Collins M.D.; Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. G. Tin. Microbiol. 31:2255-2262(1993). FEMBL; X70814; CAA50145.1; -. HSSP; P10845; 3BTA.
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MEDLINE=94013372; PubMed=8408542;
Gampbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
HSSP; P10845; 3BTA.
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                            Bacteria, Firmicutes, Bacillus/Clostridium group, Clostridia, Clostridiales, Clostridiades, Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%; Score 58; DB 2; Length 361; 64.3%; Pred. No. 0.16;
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361 361
361 AA, 42131 MW, A2EOFFFC81F9533D CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annota
Botulinum neurotoxin type B (Fragment).
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2000 (TrEMBLrel. 15,
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290 FLDFSVSFWIRIPK 303
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290 FLDFSVSFWIRIPK 303
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Clostridium botulinum.
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Q9X708;
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CLUTE. MIDGEDIOL. 29:101-110 (1994).

CLUTE. MIDGEDIOL. 29:101-110 (1994).

CLUTE. CAN MOVE BETRECGRADE TAXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INTHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERTIDASE THAT CLEAVES SYNAPTOBREVIN-2.

CLICATION OF THE HEAVY CHAIN (L) AND A A HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

CLICATION OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

CLICATION OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

CLICATION OF THE HEAVE STATE CHANNEL FORMS OF BOTULINUM NEUROTOXINS AND WITH TETANUS CLICATION.

CLICATION OF THE WITH OTHER BOTULINUM NEUROTOXINS AND WITH TETANUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO OTHER ZINC METALLOPROTEINASES IN THE ACTIVE SITE
                                                                                                                                                                                                                                                                                                                                  Hutson R.A., Collins M.D., East A.K., Thompson D.E., "Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum type B neurotoxin: comparison with other clostridial neurotoxins.";
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                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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Pred. No. 0.6;
                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Botulinum neurotoxin type B (EC 3.4.24.-) (BONT/B).
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Last annotation update)
                       1291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 AA
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                       PRT;
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Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; BONTOXILYSIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000395; Bontoxilysin.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=EKLUND 17B ATCC25765;
MEDLINE=94122659; Pubmed=7764370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X71343; CAA50482.1; -.
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Best Local Similarity 64.3
Matches 9; Conservative
                       PRELIMINARY;
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                                                                                                                                                                     Clostridium botulinum.
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                                                                                                                                                                                                                               NCBI_TaxID=1491;
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                                                                                                SEQUENCE FROM N.A.
STRAIN=593, AND 588;
Kirma N., Ferreira J.L., Baumstark B.R.;
Karama N., Ferreira J.L., Baumstark B.R.;
Characterization of six type A strains of Clostridium botulinum that contain type B toxin gene sequences.";
Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A7300466; AAL11499.1;
EMBL; A73004665; AAL11499.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Santos-Buelga J., Collins M.D., East A.K.; "Characterization of the genes encoding the Botulinum neurotoxin
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                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Pred. No. 0.6;
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Pred. No. 0.6;
4; Mismatches 1; Indels
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PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1291 AA; 150840 MW; E4D3B0E46AB2E735 CRC64;
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Last annotation update)
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01742; Peptidase M27; 1.
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InterPro; IPR000130; Zn MTpeptdse.
Pfan; PP01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXILYSIN.
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MEDLINE=98440323; PubMed=9767710;
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64.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.38;
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FLDFSVSFWIRIPK 936
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FLDFSVSFWIRIPK 936
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Best Local Similarity 64.3
Matches 9; Conservative
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Clostridium botulinum
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                                                              NCBI_TaxID=1491;
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SEQUENCE FROM N.A.
STRAIN=LCL 095;
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"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
J. Clin. Microbiol. 31:225-462(1993).
HSSP; P10845; 3BTA.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1491;
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                                                                                                                                                                                                                                  50.0%; Score 56; DB 2; Length 367; 53.8%; Pred. No. 0.36; Live 5; Mismatches 1; Indels
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53.8%; Pred. No. 0.36;
tive 5; Mismatches 1; Indels
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367 367 367 346A610C2FF70262 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last annotat
Botulinum neurotoxin type E (Fragment).
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                             MEDLINE=94013372; PubMed=8408542;
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297 YKNFSISFWVRIP 309
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297 YKNFSISFWVRIP 309
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BONT/E.
Clostridium butyricum.
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FROM N.A.
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045862
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Gyobu Y., Yamakawa K., Kato H., Nakamura S., Karasawa T.; "C. butyricum (LCL 155) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
Karasawa T.;
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
Karasawa T.;
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
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Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
Karasawa T.;
Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "C. butyricum (KZ 1899) gene for type E botulinum toxin."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                     "C. butyricum (LCL 095) gene for type E botulinum toxin.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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STRAIN=BL 6340/ATCC 43755/BL 5520/KZ 147;
MEDLINE=20509829; PubMed=11055954;
Mang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.,
"Genetic Analysis of Type E Botulinum Toxin-Producing Clostridium butyricum Strains.";
Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
Karasawa T.;
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Pred. No. 1.3;
5; Mismatches 1; Indels
                                                            "C. butyricum (LCL 063) gene for type E botulinum toxin.";
Submitted (JAN-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037714; BAB03522.1; --
EMBL; AB037704; BAB03512.1; --
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EMBL; AB039264; BAB12249.1; -.

EMSP; P10845; 3BTA.

InterPro; IPR0001395; Bontoxilysin.

InterPro; IPR000130; Zn MTpeptdee.

Pfam; PF01742; Peptidase_M27; 1.

Probom; PD001463; BONTOXILYSIN.

Probom; PD001463; BONTOXILYSIN.

PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.

SEQUENCE 1255 AA; 143918 MW; 1B557B9D8SCD8E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOXIIYSIN.
ProDom; PD001963; BONTOXIIYSIN.
PROSITE; PS001442; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1251 AA; 143751 MW; 2021F4E427070296 CRC64;
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InterPro; IPR000130; Zn_MTpeptdse.
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EMBL; AB037712; BAB03520.1; --
EMBL; AB037713; BAB03521.1; --
HSSP; PlO845; 3BTA.
MEROPS; M27.002; --
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53.8%;
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                                                                                                                                                                         EMBL, AB037705; BAB03513.1;
EMBL, AB037706; BAB03514.1;
EMBL, AB037707; BAB03515.1;
EMBL, AB037708; BAB03516.1;
EMBL, AB037708; BAB03517.1;
EMBL, AB037710; BAB03518.1;
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912 YKNFSISFWVRIP 924
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915 ***XNFSISFWVRIP 927
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Matches 7; Conservative
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Search completed: July 22, 2003, 08:11:31 Job time : 4.11464 secs

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OM protein - protein search, using sw model

July 22, 2003, 08:05:49; Search time 1.05732 Seconds (without alignments) 1909.378 Million cell updates/sec Run on:

US-09-806-703A-14

112 1 FNNFTVSFWLRVPKVSASHLE 21 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
?: pir2:\*
: pir3:\*
: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|             | nescription | tentoxilysin (EC 3 | botulinum neurotox | neurotoxin type F |        | neurotoxin type F |        | bontoxilysin (EC 3 | bontoxilysin (EC 3 | non-proteolytic bo | neurotoxin type E | botulinum neurotox | botulinum neurotox | botulinum neurotox | nucleocapsid prote | nonstructural prot | nonstructural prot | toxin, nontoxic co | botulinum neurotox | hypothetical prote |        | botulinum neurotox | botulinum neurotox | botulinum neurotox | botulinum neurotox | protein F14B6.6 [i | hypothetical prote | probable alpha-amy | hypothetical prote | gene CD5 protein - |
|-------------|-------------|--------------------|--------------------|-------------------|--------|-------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES   | TD          | BICLIN             | S33411             | S48110            | S48109 | 140813            | S39791 | BTCLAB             | A48940             | 140631             | S48106            | JH0256             | S21178             | I40645             | S23158             | MINVUWC            | MNVUW1             | JQ1467             | S46430             | T33493             | T47446 | S70582             | S46431             | A49777             | S11455             | F87937             | T20879             | B37837             | T25966             | 147074             |
| 9           | 9           | Н                  | 7                  | ~                 | 7      | N                 | ~      | П                  | Н                  | ~                  | ~                 | ~                  | ~                  | N                  | ~                  | Н                  | -                  | ~                  |                    | 7                  |        |                    |                    | ~                  | ~                  | ~                  | 7                  | ~                  | ~                  | 7                  |
| ,<br>,<br>, | rengen      | 1315               | 1268               | 366               | 369    | 1274              | 1297   | 1296               | 1291               | 1291               | 367               | 1251               | 1252               | 1296               | 449                | 464                | 467                | 1196               | 1196               | 276                | 504    | 1285               | 1291               | 1291               | 1276               | 359                | 385                | 469                | 322                | 442                |
| %<br>Query  | marcn       | 100.0              | ı,                 | 54.5              | ٠      | 4                 |        | ď                  | 51.8               | 51.8               |                   |                    |                    | 50.0               | 46.4               | 46.4               |                    |                    |                    | 43.8               | •      | ٠                  |                    | 42.9               | 42.4               |                    |                    | 42.0               | 41.1               | 41.1               |
| 9           | acore       | 112                | 62                 | 61                | 61     |                   |        | 59                 | 58                 | 58                 | 26                | 99                 | 56                 | 99                 | 25                 | 52                 | 52                 |                    | 51                 | 49                 | 48     | 48                 | 48                 | 48                 | 47.5               | 47                 | 47                 | 47                 | 46                 | 46                 |
| esult       |             | -                  | 7                  | e                 | 4      | ហ                 | ø      | 7                  | ω                  | σ                  | 10                | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20     | 21                 | 22                 | 23                 | 24                 | 22                 | 26                 | 27                 | 28                 | 29                 |

| probable myb-like | unknown protein Fl | progenitor toxin n | botulinum toxin no | hypothetical prote | hypothetical prote | conserved hypothet | enterochelin ester | spheroidene monoox | probable membrane | hypothetical prote |        | _      | _      | _      |        |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------|
| T38197            | C96668             | A47708             | 140817             | T41362             | T39081             | A82470             | AD0574             | S04401             | D64943            | B99945             | E85793 | A90711 | E85561 | T20858 | F83884 |
| Ŋ                 | N                  | 7                  | N                  | N                  | 7                  | ~                  | N                  | N                  | ~                 | N                  | 7      | 7      | N      | ~      | 7      |
| 496               | 753                | 1162               | 1162               | 528                | 988                | 209                | 404                | 591                | 152               | 152                | 152    | 381    | 381    | 514    | 781    |
| 41.1              | 41.1               | 41.1               | 41.1               | 40.2               | 40.2               | 39.3               | 39.3               | 39.3               | 38.4              | 38.4               | 38.4   | 38.4   | 38.4   | 38.4   | 38.4   |
| 46                | 46                 | 46                 | 46                 | 45                 | 45                 | 44                 | 44                 | 44                 | 43                | 43                 | 43     | 43     | 43     | 43     | 43     |
| 30                | 31                 | 32                 | 33                 | 34                 | 32                 | 36                 | 37                 | 38                 | 39                | 40                 | 41     | 42     | 43     | 44     | 45     |

# ALIGNMENTS

| RESULT 1                               |  |
|--|--|
| BICLIN                                 |  |
| tentoxilysin (EC 3.                    | tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani                                 |
| N;Alternate names: tetanus neurotoxin  | nus neurotoxin   |
| C; Species: Clostridium tetani         | tetani   |
| C;Date: 31-Mar-1988                    | C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 03-Jun-2002                |
| C;Accession: A25689                    | C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364                        |
| R; Eisel, U.; Jaraus                   | R; Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M., |
| EMBO J. 5, 2495-2502, 1986             | . 986  |
| A; Title: Tetanus to                   | A; Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botul |
| A;Reference number:                    | A; Reference number: A25689; MUID:87053814; PMID:3536478                                   |
| A;Accession: A25689                    |  |
| A;Molecule type: DNA                   |  |
| A, Residues: 1-1315 <eis></eis>        | ^  |
| A; Cross-references:                   | A; Cross-references: GB:X04436; NID:q40769; PIDN:CAA28033.1; PID:q40770                    |
| R; Fairweather, N.F.; Lyness, V.A.     | ness, V.A.   |
| Nucleic Acids Res. 14, 7809-7812, 1986 | 7609-7812, 1986  |
| A; Title: The comple                   | A, Title: The complete nucleotide sequence of tetanus toxin.                               |
| A; Reference number:                   | A; Reference number: A25757; MUID:87040747; PMID:3774547                                   |
| A; Accession: A25757                   |  |
| A;Molecule type: DNA                   |  |
| A; Residues: 1-1315 <fai></fai>        | ٨  |
| A; Cross-references:                   | A;Cross-references: GB:XC6214; NID:g40773; PIDN:CAA29564.1; PID:g40774                     |
| A, Experimental source: strain CN3911  | strain CN3911  |
| R; Fairweather, N.F.                   | R;Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.                 |
| J. Bacteriol. 165, 21-27, 1986         | 7, 1986  |
| A, Title: Cloning, n                   | A; Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in Es |
| A;Reference number:                    | A;Reference number: A25194; MUID:86085672; PMID:3510187                                    |
| A;Accession: A25194                    |  |

A,Accession: A25194
A,Molecule type: DNA
A,Residues: 743-1315 <FA2>
A,Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921
A,Accession: B25194

A,Molecule type: protein
A,Molecule type: protein
A,Residues: 865-894 <FA3>
R,Matsuda, M.; Leb, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A,Title: Isolation, purification, and characterization of fragment B, the NH-2-terminal B, A,Accession. A60759; MUD: 90035436; PMID: 2478476
A,Accession. A60759
A,Molecule type: protein
A,Residues: 461-475 <MAT>
R,Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989
A,Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A,Feference number: 150098; MUD: 8909318; PMID: 2463305
A,Contents: annotation; epitope region
R,Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.
Nature 359, 832-835, 1992
A,Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyti
A,Reference number: S27125; MUD: 93063293; PMID: 1331807
A,Contents: annotation

N

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Gaps

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CAccession: $48109
R;Campbell, K.D.; Collins, M.D.; East, A.K.
Campbell, K.D.; Collins, M.D.; 2255-2262, 1993
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific ide
A;Reference number: $48103, MUID: 94013372; PMID: 8408542
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1274 eREN
A;Cross-creferences: GB:M92906; NID:g144866; PIDN:AAA23263.1; PID:g144867
B;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Ciln. Microbiol. 31, 2255-2262, 1993
A;Fitle: Gene probes for identification of the botulinal neurotoxin gene and specific ide
A;Reference number: S48103; MUID:94013372; PMID:8408542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E. FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A;Reference number: I40644
A;Accession: 140813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X70820; NID:g407790; PIDN:CAA50151.1; PID:g407791
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurotoxin type F - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: i2-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurotoxin type F - Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: 140813; S48108
                      A;Cross-references: EMBL:X70821; NID:g407792; PIDN:CAA50152.1; PID:g407793 C;Superfamily: tetanus toxin C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Residues: 634-1002 <CAM>
A.Residues: 634-1002 <CAM>
A.Cross-references: EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PID:g407789
C.Superfamily: tetanns rowin
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Pred. No. 0.11;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 369;
                                                                                                                                                         Length 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 2;
Pred. No. 0.029;
                                                                                                                                                         Score 61; DB 2;
Pred. No. 0.028;
                                                                                                                                                                                                                    5; Mismatches
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                                                                                                                                                         54.5%;
57.1%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                         : ||::|||:||
297 YQNFSISFWVRIPK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||::||:||
297 YQNFSISFWVRIPK 310
                                                                                                                                                                                                                                                                                  1 FUNFTVSFWLRVPK 14
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                                                                                                                                                      Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-369 < CAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: S48108
   A;Residues: 1-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dotulinum neurotoxin type F - Clostridium barati
C;Species: Clostridium barati
C;Species: Clostridium barati
C;Species: 13-40-1995 #Sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: 333411; S31860
R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
FEMS Microbiol. Lett. 108, 175-182, 1993
A;Title: Nucleotide sequence (the gene coding for Clostridium barati type F neurotoxin A;Reference number: S33411; MUID:93252228; PMID:8486245
A;Accession: S33411
A;Scatus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                              C; Comment: The source of this protein was an extrachromosomal plasmid.

C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra dual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C; Comment: Fragment B forms ion channels in a lipid bipayer. Fragment C binds to ganglid C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                                                                                                                                                                                                                                                                                                                                                                                                     C, Function:
A) the scription: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt C, Superfamily: tetanus toxin
C, Superfamily: tetanus toxin
C, Superfamily: tetanus toxin
C; Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F, 2-457/Product: tentoxylysin light chain (fragment A) #status predicted <TTL>
F, 461-1315/Product: tentoxylysin heavy chain (fragment B) C) #status experimental <TTH>
F, 461-864/Domain: channel forming (fragment B) #status predicted <TXB>
F, 865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>
F, 233, 237/Binding site: zinc (His) #status predicted
F, 234/Active site: Glu #status predicted
                             Eur. J. Biochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.
A;Reference number: S69348; MUID:95262688; PMID:7744050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S48110

neurocroxin type F - Clostridium botulinum (fragment)

c;Species: Clostridium botulinum

c;Date: 14-Unl-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C;Accession: S48110

C;Accession: S48110

C;Accession: S48110

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific in Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific in Microsion: S48110

A;Recession: S48110

A;Accession: S48110

A;Accession: S48110

A;Molecule typq: DNA
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Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1268 <THO>
A;Cross-references: EMBL:X68262; NID:g49138; PIDN:CAA48329.1; PID:g49139
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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Pred. No. 0.073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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YQNFSVSFWVRIPK 935
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1es 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                     A, Accession: S69348
A, Molecule type: protein
A, Residues: 2-31 <DEF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 9; Conserv
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Best Local S
Matches 9
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A; Molecule type: protein
A; Residues: 867-880;1148-1217,'Y',1219 <GIM>
A; Residues: 867-880;1148-1217,'Y',1219 <GIM>
A; Experimental source: strain Hall
A; Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after ext
R; DasGupta, B.R.; Dekleva, M.L.
Biochimie 72, 661-664, 1990
A; Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and arour
A; Reference number: A60025; MUID:91120847; PMID:2126206
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N;Alternate names: botulinum neurotoxin type B (BoNT/B)
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text change 18-Jun-1999
C;Accession: A48940; S48105; $21575; A42871; S07155; S08562; S07128; S08573; S08574
R;Whelan, S.M.; Elmore, M.J.; Bodaworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the type
A;Reference number: A48940; MUID:92384550; PMID:1514783
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A; Residues: 1-1291 < WHES
A; Crossines: 1-1291 < WHES
A; Crossines: 1-1291 < WHES
A; Crossines: 1-1291 < WHES
A; Crossines: 1-1291 < WHES
A; Experimental source: type B, Danish
A; Experimental source: type B, Danish
A; Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this publicat
R; Campboll, X; D; Colling, M. D; East, A. K.
A; Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and specific ide
A; Reference number: S48103; MUID:94013372; PMID:8408542
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   R;Gimenez, J.A.; DasGupta, B.R.
L. Proteain Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45,
A;Reference number: A53884; MUID:94000342; PMID:8397793
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Modecule type: protein
A,Residues: 2-6;445-453, XX, 455-457 <DAS1>
R;DasGupta, B.R.; Poley, J.; Niece, R.
Bicchemistry 26, 4162, 1997
A;Title: Partial sequence of the light chain of botulinum neurotoxin type.
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A,Residues: 2-47 cDAS2>
R;Binz, T;Blasi, J; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof,
J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49703; MUID:94124495; PMID:8294407
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Pred. No. 0.24;
4; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative
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A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-12 <FUJ>
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: DNA
A.Status: DNA
A.Status: DNA
A.Status: DNA
A.Status: Commun: 162, 1388-1395, 1989
A.Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term
A.Reference number: A33401; MUD:89350959; PMID:2669749
A.Accession: A33401
A.Molecule type: DNA
A.Residues: 1.35 <ABT>
A.Status AAAA23269.1; PID:9551776
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BONLOXIlysin (EC 3.4.24.69) A precursor - Clostridium botulinum

Nathernate names: botulinum neurotoxin type A

C;Alestidium botulinum

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text change 18-Jun-1999

C;Accession: A35.294; 809492; $68220; A33401; A53884; A60025; A27000

R;Binz, T. R. Karazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.

J. Biol. Chem. 265, 9153-9158, 1990

A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other
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A; Residues: 1-1296 ABIN>
A; Cross-references: GB:M30196; NID:g144864; PIDN:AAA23262.1; PID:g144865
A; Cross-references: GB:M30196; NID:g144864; PIDN:AAA23262.1; PID:g144865
A; Experimental Source: strain GA, subtype A
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T. Bur. J. Biochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin A; Reference number: S09492; MUID:90235864; PMID:2185020
                                                                                                                                         RESULT 6
339791

Boundoor Constriction Detailinum
C;Species: Clostriction Detailinum
C;Species: Clostriction Detailinum
C;Species: Clostriction Detailinum
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
R;Campbell, K.; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta 1216, 487-491, 1993
A;Title: Nuclectide sequence of the gene coding for Clostridium Detailinum (Clostridium A;Reference number: S39791; MUID:94092745; PMID:8268233
A;Accession: S39791
A;Status: preliminary
A;Actaus: preliminary
A;Actaus: July A;Actaus DNA
A;Dataus: July A;Actaus DNA
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A;Dataus DNA
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A;Reference number: S67988; MUID:96096783; PMID:8521962
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A;Cross-references: EMBL:X74162; NID:g441275; PIDN:CAA52275.1; PID:g441276
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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A;Residues: 1,'0',3-26,'V',28-1296 <THO>
A;Cross-references: EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID:g40382
A;Experimental source: NCTC 2916
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FBBS Lett. 376, 41-44, 1995
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Pred. No. (
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FDNFSINFWVRTPKYNNNDIQ 950
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930 YQNFSISFWVRIPK 943
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Best Local Similarity
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C,Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
C;Accession: I40631; S48103; S48104; S36015
C;Accession: I40631; S48103; S48104; S36015
C;Accession: I40631; S48103; S48104; S36015
Curr. Microbiol. 28, 101-110, 1994
A;Title: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum A;Reference number: I40631; MUID:94122659; PMID:7764370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 634-843,'T',845,'N',847-994 <CAM2>
A;Cross-references: EMBL:X70819, NID:9407780; PIDN:CAA50150.1; PID:9407781
A;Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C;Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic s,
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A;Residues: 634-761, E',763-841, M',843,'T',845,'N',847-994 <CAMI>
A;Cross-references: EMBL:X70814; NIDS401778; PIDN:CAA50145.1; PID:g407779
A;Experimental source: non-proteolytic strain 2129B (Scott)
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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C;Keywords: metalloprotein; neurotoxin; transmembrane protein; zinc
C;Keywords: metalloprotein; neurotoxin type B light chain #status predicted <LGHT>
F;442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVY>
F;230,234/Binding site: zinc (His) #status predicted
F;231/Active site: Glu #status predicted
                                                                                                                                           non-proteolytic botulinum neurotoxin type B precursor - Clostridium botulinum
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R; Campbell, K.D.; Collins, M.D.; East, A.K.
G; Cilm. Microbiol. 31, 2255-2266, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and A; Reference number: S48103; MUID: 94013372; PMID:8408542
A; Status: S48106
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Clostridium botulinum
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
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ollins, M.D.; East, A.K.
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Clin, Microbiol, 31, 2255-2262, 1993
;Title: Gene probes for identification of the botulinal
;Reference number: S48103; MUID:94013372; PMID:8408542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cresidues: 1-1291 exES-
A;Cresidues: 1-1291 exES-
R;Campbell, K.D.; Collins, M.D.; East, A.K.
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FLDFSVSFWIRIPK 936
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les 9; Conservative
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A; Residues: 1-367 < CAM>
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A; Modecule type: protein
A; Modecule type: protein
A; Residues: 442-459 < SCH3>
R; Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.
R; Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.
Nature 359, 832-835, 1952
A; Fitle: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
A; Contents: annotation
C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
C; Genetics:
A; Gene: bont/b
C; Function:
A; Gene: bont/b
C; Function:
C; Moderially: tetanus toxin
C; Moyords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
C; Moyords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
C; Moyords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
C; Moyords: hydrolase; metalloproteinase; neurotoxin; transmembrane LGHT>
F; 2-19-1/Product: bontoxilysin B heavy chain #status experimental < HVY>
F; 231/Active site: Glu #status predicted
A; Molecule Cype: DNA
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Residues: 634-994 < CAM>
A; Experimental Source: proteclytic type B, strain NCTC 7273
A; Exabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
B; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
A; Reference number: 821575
A; Reference number: 821575
A; Reference number: 821575
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 196-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 196-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 199-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Residues: 36-217, G', 219-224, S', 226-246 < SZA>
A; Ridia Ciminal essential domains specifying toxicity of the light chains of tetanus to A; Reference number: A2871; MUD: 92346509; PMID: 1634516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Affile: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A;Reference number: S07155; MUD:89000987; PMID:3139097
A;Reference number: S07155; MUD:89000987; PMID:3139097
A;Accession: S08552
A;Residues: 2-29, 'M', 31-45 < DAS>
A;Residues: 2-29, 'M', 31-45 < DAS>
A;Residues: 442-463, 'R', 465-467 < DA2>
A;Residues: 442-463, 'R', 465-467 < DA2>
A;Residues: 442-463, 'R', 465-467 < DA2>
A;Residues: 442-463, 'R', 465-467 < DA2>
A;Residues: 528, 544-548, 1985
A;Title: Partial amino acid sequences of botulinum neurotoxins types B and E.
A;Reference number: S07128; MUD:85197963; PMID:3888113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-313, 'S', 315-451 «KUR»
A; Experimental source: strain Okra
A; Note: sequence extracted from NCBI backbone (NCBIP:109365)
B; DasGupta, B.R.; Datta, A.
Biochimie 70, 811-817, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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64.3%;
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 2-16 <SCH1>
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A;Residues: 2-17 <SCH2>
A;Accession: S08574
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Best Local Similarity
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A; Status: preliminary
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Gapa

DB 2; Length 367;

50.0%; Score 56;

Query Match

923 FLDFSVSFWIRIPK 936

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Tue Jul

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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-176,'R',178-197,'C',199-339,'R',341-772,'I',774-962,'FE',965-966,'R',968-11
A;Cross-references: EMBL:X62089; NID:g40393; PIDN:CAA43999.1; PID:g40394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ridimenez, J.A.; DasGupta, B.R. B.B. Biochimie 72, 213-217, 1950 Biochimie 72, 213-217, 1950 A.F. B. Eragmented with endoproteinase Lys-C reveals the sit A;Reference number: A60027; MUID:90344918; PMID:2116911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Experimental source: strain Beluga
A;Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neur
C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the ligh
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
      A;Cross-references: EMBL:X70815; NID:g407786; PIDN:CAA50146.1; PID:g407787

Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.

Biochem. Biophys. Res. Commun. 183, 107-113, 1992

A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type A;Reference number: JH0256; MUID:92181428; PMID:1543481
                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain Beluga
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
A; Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; MUID:90264400; PMID:2160960
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
C;Accession: 140645
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Pred. No. 0.75;
5; Mismatches 2; Indels
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A;Title: Sequence of the gene coding for the neurotoxin A;Reference number: I40645; MUID:94143603; PMID:8310180
A;Accession: I40645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           botulinum neurotoxin type A - Clostridium botulinum
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Pred. No. 0.72;
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A;Molecule type: DNA
A;Residues: 1-1296 <RES>
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938 YENFSTSFWIKIPK 951
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912 YKNFSISFWVR.IP 924
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nes 7; Conserv
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Matches 7
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                                                                                                                                                                                                                                                              RESULT 11

JH0256

botulinum neurotoxin type E precursor - Clostridium butyricum

C;Species: Clostridium butyricum

C;Species: Clostridium butyricum

C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 16-Jul-1999

C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 16-Jul-1999

R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.

Biochem. Biophys. Res. Commun. 183, 107-113, 1992

A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type

A;Reference number: JH0256; MUID:92181428; PMID:1543481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-27, 'E',29-125; VE',29-125;
A;Cross-references: BMBL:X62088; NID:940379
A;Erbii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N.
J. Gen. Microbiol. 137, 519-525, 1991
A;Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxi
A;Reference number: S16145; MUD:91237316; PMID:2033376
A;Accession: S16145
A;Accession: S16145
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S21178
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X62683; NID:g40397; PIDN:CAA44558.1; PID:g40398
B;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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botulinum neurotoxin type E precursor - Clostridium botulinum

c;Species Clostridium botulinum botulinum

c;Species 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 15-Oct-1999

c;Accession: $21178; $48107; JH0257; $35294; A60027; $18111

E;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P.

Bur. J. Blochem. 204, 657-667, 1992

A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin

A;Reference number: $21178; MUID:92174922; PMID:1541280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig C;Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Keywords: neurotoxin
F;2-422/Product: botulinum neurotoxin type E light chain #status predicted <LIG>
F;423-1251/Product: botulinum neurotoxin type E heavy chain #status predicted <HEA>
F;412-426/Disulfide bonds: #status predicted
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A;Cross-references: EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PID:g40408
A;Experimental source: strain BL6340
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                                         Mismatches
          Pred. No.
      ilarity 53.8%;
Conservative
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297 YKNFSISFWVRIP 309
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A;Residues: 616-982 <CAM>
Best Local Similarity
Matches 7; Conserv
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RESULT 14 S23158

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A;Cross-references: EMBL:X66972; NID:g60488; PIDN:CAA47382.1; PID:g60489
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 104-Val
C;Superfamily: tomato spotted wilt virus nonstructural protein NS
C;Keywords: nucleocapsid
nucleocapsid protein - Impatiens necrotic spot virus
C;Species: Impatiens necrotic spot virus
C;Species: Impatiens necrotic spot virus
C;Species: Impatiens necrotic spot virus
C;Species: Impatiens necrotic spot virus
C;Species: Impatiens necrotic spot virus
C;Accession: S23158
R;de Haan, P.; de Avila, A.C.; Kormelink, R.; Westerbroek, A.; Gielen, J.J.L.; Peters, I FEBS Lett. 306, 27-32, 1992
A;Title: The nucleotide sequence of the S RNA of Impatiens necrotic spot virus, a novel
A;Reference number: S23158; MUID:92331780; PMID:1385787
A;Accession: S23158
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-449 <HAA>
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46.4%; Score 52; DB 2; Length 449;
Best Local Similarity 45.0%; Pred. No. 1.1;
Matches 9; Conservative 5; Mismatches 4; Indels
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RESULT 15
MNVUWC

NONSTRUCTURAL PROTEIN NS - tomato spotted wilt virus (strain CPNH1)

C;Species: tomato spotted wilt virus
C;Species: tomato spotted wilt virus
C;Species: tomato spotted wilt virus
C;Accession: JQ0547
R;Ge Haan, P: Wagemakers, L; Peters, D.; Goldbach, R.
R;Ge Haan, P: Wagemakers, L; Peters, D.; Goldbach, R.
R;Gen: Virol. 71, 1001-1007, 190
A;Title: The S;RNA segment of tomato spotted wilt virus has an ambisense character.
A;Reference number: JQ0547; MUD:90264829; PMID:1693160

240 NNKPFKISLWMRIPKIMKSN 259 NN--FTVSFWLRVPKVSASH 19

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A;Cross-references: DDBJ:D00645; NID:g222685; PIDN:BAA00540.1; PID:g222686 C;Genetics: A; Molecule type: genomic RNA A; Residues: 1-464 <DEH> A; Gene: NS

A;Map position: segment S C;Superfamily: tomato spotted wilt virus nonstructural protein NS C;Keywords: glycoprotein; nonstructural protein F;132,210,270,291,381/Binding site: carbohydrate (Asn) (covalent) #status predicted Score 52; DB 1; Length 464; Pred. No. 1.2; 3; Mismatches 2; Indels 46.48; Best Local Similarity 64.3%; Matches 9; Conservative

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Gaps ö

> ::| :| |||||||| 239 SHFKLSLWLRVPKV 252 2 NNFTVSFWLRVPKV 15 ð 셤

Search completed: July 22, 2003, 08:12:44 Job time : 2.05732 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES DB ID Description   | 21 AAY92620 Human heregulin 2 | 22 AAE12130 | 22 AAB60167 | 23 AAU74545 Human HER2 (ErbB2) | 17 AAW01111 | 20   | 21 AAB21198 | 21 AAY84780 | 22 AAB85458 | 22 AAG88267 |
|-------------------------------|-------------------------------|-------------|-------------|--------------------------------|-------------|------|-------------|-------------|-------------|-------------|
| ,<br>h DB                     | 5 21                          | 5 22        | 5 22        | 5 23                           | 5 17        | 5 20 | 5 21        | 5 21        | 5 22        | 5 22        |
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| Score                         | 6812                          | 6812        | 6812        | 6812                           | 6806        | 9089 | 9089        | 9089        | 9089        | 6806        |
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Length 1255;

DB 21; .. 0 9 9 120

180 180 240 240 300 300 360 360 420 420 480 480 540 540 900 900 99 99 720 720 780 780

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cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PA), herequilin Z (Herz) and/or fibroblast growth factor Bb (FGFBb). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA, and (2) at least 1 B-cell group derived from the cell-associated PA, and (2) at least 1 B-cell group which is foreign to the animal. Analogues of human PSM, human Herz and human/murine FGFBb comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGFBb and Herz, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPIDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                                 Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines of the expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and pl85neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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is characterised by the overexpression of an epidermal growth factor receptor (ETbB) and does not respond or responds poorly, to treatment with an anti-ETbB antibody, comprising administering to the mammal an anti-ETbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ETbB2. The method is also useful for treating encroal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                       EEYLVPQQGFFCPDPAPGAGGWVHRRRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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             Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                                                                 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGGLVDA
                                                                                                                                                                                                                                            EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                                                                                                                                                                       AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                                                                                                                                                                                                                NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                                                                                                                                                                                                                                                     IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                                          LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                       HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
676..1255
/label Intracellular domain
/note= "claimed domain, useful for immunisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 56-61; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 1255
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N-PSDB; AAT40739.
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|---|---|--|---|
| qq  | 772 ILGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLNWGVQIAKGMYYLEEHSMVHR 831  | q  | 117 GLEGCPHGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172   |
| ,<br>,  | VKSPNHVKITDFG   | ò  | 691 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLR 750  |
| qa  | 832 DIALRNVMLKSPSGVQVADFGVADLLPPDDKQLLHSBAKTPIKWMALESIHFGKYTHQSD 891  | අු   | 173 VEPLTPSGEAPNQAHLRILKETEFKKVKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELR 232  |
| o da  | 899 VWSYGVTVWELMTFGAKPYDGIPAREIPDLIEKGERLPQPPICTIDVYMINVKCMMIDSE 958  | \$ 93  | 751 ENTSPKANKEILDEAYVRAGVGSPYVSRLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 810 233 EATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDN 292  |
| & 8   | 959 CRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDABEYL 1018   | 6 64<br>64   | 811 LGSQDLIAWGWQIAKGMSYLEDVRIVHRDLAARNVIVKSPNHVKITDFGLARLLDIDETE 870<br>  |
| 5 G   | 1019 VPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEB 1062  | දු පු  | 871 YHADGGKVPIKWMALESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLE 930<br>   :  |
| 0,  | 1063EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDP 1110   | ٥٨   | 931 KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG 989  |
| Dp .  | 1035 LTRPRGSQSLLSPSSGYMPMNQSSLGEACLDSAVLGGREQFSRPISLH-PIPRGR 1088   | ΟD   | 413 KGERLPÓPPÍCTÍDVYMÍMVKCWMÍDADSRÞKFRELIAEFSKWARDPPRYLVÍQGDERMH 472  |
| Oy<br>Db  | 1111 TVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGP 1150  | <u>ئ</u> ۾   | 990 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1049<br>   |
| 0y 1  | 1151  | 60 8   | 1050 GGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1104   |
| cy<br>do  | 1193 PQGGAAPQPHPP 1204<br>: :         <br>1199 RKRRGSP-PRPP 1209  | çy<br>Dp   | 1105 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE 1162  |
| RESULT 11   |   | કે ઇ   | 1163 RAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAF 1207   |
| protein-ty<br>N;Contains<br>C;Species:<br>C;Date: 31                    | protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase C;Species: avian leukosis virus, ALV C;Species: avian leukosis virus, ALV C;Decies: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999                                  |  | SPAFDNLYYWDQDPPERGAPPSTFKGTFTAENPEYLGLDVP 1246  ::               XTVFESSPYWIQSGNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP 689   |
| C; Accessic<br>R; Nilsen,   | on: BU0643; AU0643<br>T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M<br>719-726, 1985   | RESILL 12  |   |
| A;Title: A;Reference A;Accessic A;Molecule                              | nd pro  | TVYUH protein-t C;Species C;Date: 1                                | yrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H) : avian erythroblastosis virus virus (strain H) 8-Apr-1984 #sequence revision 18-Apr-1984 #text change 11-Jun-1999   |
| A, Residue: A, Cross-re A, Note: ir C, Comment:                         | 0<br>us gal   | C; Accessi<br>R; Yamamot<br>Cell 35,<br>A; Title:                  | on: A00644; A36022 -<br>Co. T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.<br>71-78, 1983 - Anna Frythroblastosis virus is a member of the src gene famil   |
| C, Genetica<br>A, Gene: ga<br>C, Superfan<br>C, Keyworda<br>F, 1-6/Proc | C;Genetics: A;Gene: gag-env-erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP: oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;1-6/Product: gag protein (fragment) #status predicted <gag></gag> | A; Referer<br>A; Accessi<br>A; Molecul<br>A; Residue<br>A; Cross-r | A;Reference number: A00644; MUID:84026539; PMID:6313229 A;Accession: A00644 A;Molecule Pype: DNA A;Residues: 1-604 <yam> A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678</yam>   |
| F;7-59/PK<br>F;60-698/1<br>F;194-459/<br>F;202-210/<br>F;229/Acti       |   | R;Debuire<br>Science 2<br>A;Title:<br>A;Referen<br>A;Accessi       | 2, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, A., 1456-1459, 1984 Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of ne number: A38022; MUID:84223957; PMID:6328658 con: A38022.                    |
| Query Ma<br>Best Loc<br>Matches   | tch 26.1%; Score 1766.5; DB 1; Length 698; al Similarity 52.2%; Pred. No. 2.3e-65; 374; Conservative 80; Mismatches 137; Indels 125; Gaps 18;   | A; Molecul<br>A; Residue<br>A; Cross-r<br>C; Genetic               | <pre>c type: DNA c type: DNA se: 1-28, W', 30-139, F', 141-145, 'V', 147-152 &lt; DEB&gt; eferences: GB: K02006 is: 15: 15: 15: 15: 15: 15: 15: 15: 15: 15</pre>  |
| <u>ک</u> ۾  | 572 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEBGACOPCPINCTHSCVDL 631  | C; Superfa<br>C; Keyword<br>F; 130-395                             | 'Superfamily: epidermal growth factor receptor; protein kinase homology; Superfamily: epidermal growth factor receptor; keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific; 130-398/Domain; protein kinase homology <kin></kin> |
| ò   | 632 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL 690  | F;165/Act  | oregion: process Astronomy Worse<br>live site: Lys #status predicted  |

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A; Reddues: 'Y, 832-866,'V', 868-943,'OTPSLVK' < WAD>
A; Reddues: 'Y, 832-866,'V', 868-943,'OTPSLVK' < WAD>
A; Cross-references: EMBL:X0229; NID:97922; PIDN:CAA26157.1; PID:9929565
C; Comment: This sequence is tentative because the introns have not been identified.
C; Gane: FlyBase:Egfr
A; Gross-references: FlyBase:FBgn0003731
A; Map position: 2 57F
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorylation; duplication: 2 57F
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphorylation: chracellular #status predicted <TMM>
F; 132 Domain: protein kinase homology <AINN>
F; 816-824/Region: protein kinase ATP-binding motif
F; 122,300,324,363,518,688,695,700(Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 1181/Binding site: bhosphate (Tyr) (covalent) (by protein kinase C) #status predicted
F; 1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKMYTLEIPDLRDVINGOVGFHNNYNLCHMRTIQMSEIVSNGTDAYYNYDFTAPERECPK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHESCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 LACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 AIQKEPEQKVWVNENLRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSVQRGRLL 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CHOLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYV----NARHCLP 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 SYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSCPQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH------AGNIDSFRNCTVIDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 LVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FONLOVIRGRILHNGAY-SLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 VQGYVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 ITNYIVIGLDLIPCTLSYRLQIIRGRTLFSLSVEBERYALFV-------TY
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A; Residues: 1-1330 (LIV>
A; Cross-references: EMBL: K03054
A; Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Nature: 314, 178-180, 1985
N; Title: A Drosophila genomic sequence with homology to human epidermal growth:
A; Reference number: A38021; MUID: 85137938; PMID: 2983232
                                                    16;
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;Decies: Drosophila melanogaster
C;Decies: TAMAR-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
                                                                                               CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                       CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 ICTIDVYMIMVKCWMIDADSRPKFRELIABFSKWARDPPRYLVIQGDERMHLPSPTDSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rilivneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Scall 40, 599-607, 1985.
Affiltle: The Drosophila EGF receptor gene homolog: consequence number: A00640; MUID:85124611; PMID:2982499 A; Accession: A00640
    Score 1703; DB 1;
Pred. No. 7.9e-63;
; Mismatches 128;
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| C 755  V 719  V 815  L 875  L 875  D 935  D 935  C 1143  C 1143  C 1143  C 1220  P 1220  P 1220  P 1279 | ine-specific F                           | Qy 632 DDKGCPAEQFASPLTSIVSAVV-GILLVVVLGVVFGILIKRQQKIRKYTMRRLLQETEL 690 VCQLCHPNCTRGCKGP 57 |
|---|--|--|
|   | in lin lin lin lin lin lin lin lin lin l | Db 1 GPDHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP                            |

Search completed: July 22, 2003, 09:07:45 Job time : 30.7967 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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OM protein - protein search, using sw model

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec Run on:

SEQ4-465-479-12 6804 Title: Perfect score:

1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1255 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* . . . .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description    | 571 protein-tyrosine |        |        | epidermal | 3 epidermal | epidermal | epidermal | protein-t) |        |        | protein-ty |       |        | 727 kinase-related tra |        | protein-ty |        | epidermal growt | protein le |        |        |       | epidermal | epidermal | protein-ty |        |        |        |
|-----------|----------------|----------------------|--------|--------|-----------|-------------|-----------|-----------|------------|--------|--------|------------|-------|--------|------------------------|--------|------------|--------|-----------------|------------|--------|--------|-------|-----------|-----------|------------|--------|--------|--------|
| 0,1       | ID             | A24571               | 148161 | TVRTNI | COHOE     | A53183      | TVCHLV    | A47253    | S06142     | A36223 | JC4387 | TVFVLV     | TVYUH | 835745 | 800727                 | B44776 | TVFVEB     | GOFFE  | A36325          | E88257     | S70712 | 870713 | A4558 | A42032    | A27131    | S13807     | S13808 | T43220 | TATUTE |
|           | DB             | ; ⊣                  |        |        | Н         |             | Н         |           |            |        |        | Н          |       |        |                        |        |            |        | 7               |            |        |        |       |           |           |            |        |        |        |
|           | Length         | 1255                 | 1254   | 1260   | 1210      | 1210        | 1223      | 1308      | 1166       | 1342   | 1339   | 698        | 604   | 544    | 545                    | 540    | 540        | 1330   | 644             | 1323       | 1374   | 1369   | 1717  | 527       | 843       | 346        | 311    | 1363   | 1207   |
| de        | Query<br>Match | 97.5                 | 86.0   | 85.9   | 45.9      | 45.4        | 45.2      | 43.3      | 39.1       | 35.0   | 33.8   | 26.0       |       | 24.2   | 24.1                   |        | 23.8       | 23.8   | 21.7            | 19.0       | 19.0   | 7.     | 17.2  | 16.3      | 13.9      | 11.9       | 11.1   | 10.6   | ,      |
|           | Score          | 6631                 | 5851.5 | 5844   | 3121      | 3087        | 3074.5    | 2943.5    | 2658       | 2384.5 | 2300.5 | 1766.5     | 1703  | 1647   | 1640                   | 1623   | 1621       | 1620.5 | 1479            | 1292       | 1292.  | 1196   | 1169  | 1108      | 948.5     | 806.5      | 754.5  | 724    | 707    |
|           | Result<br>No.  | 1                    | 2      | М      | 4         | ß           | 9         | 7         | 8          | σı     | 10     | 11         | 12    | 13     | 14                     | 15     | 16         | 17     | 18              | 19         | 20     | 21     | 22    | 23        | 24        | 25         | 26     | 27     | ac     |

| protein-tyrosine k | insulin receptor p | insulin-like growt | insulin receptor-r | insulin receptor-r | insulin-like growt | insulin-like growt | insulin receptor - | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | receptor tyrosine | protein-tyrosine k | protein-tyrosine k |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| T18534             | A34157             | T43212             | A36502             | B36502             | IGHUR1             | A33837             | T30346             | A56081             | S57245             | A39753             | A54092             | 150612             | 151672            | S05582             | 833596             |
| 7                  | 7                  | ~                  | 7                  | 7                  | Н                  | 7                  | ~                  | ٦                  | 7                  | 7                  | 7                  | 7                  | 7                 | Н                  | ~                  |
| 1477               | 1372               | 1607               | 1300               | 1268               | 1367               | 1371               | 1390               | 2148               | 2101               | 984                | 987                | 952                | 985               | 1114               | 1091               |
| 10.2               | 10.2               | 10.1               | 10.0               | 9.9                | 9.5                | 9.5                | 9.5                | 9.1                | 9.1                | 9.0                | 8.9                | 8.8                | 8.6               | 8.6                | 8.6                |
| 695                | 694.5              | 685                | 681.5              | 674                | 646                | 628                | 626                | 621.5              | 616                | 609.5              | 603                | 601.5              | 587.5             | 587                | 286                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 32                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                | 44                 | 45                 |

## ALIGNMENTS

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1997 #sequence revision 06-Dec-1996 #text\_change 11-Jun-1999
C;Accession: A24571; A25;91; A44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Ryture 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f A;Reference number: A24571; MUID:86118663; PMID:3003577

A; Accession: A24571

A; Molecule type: mRNA A; Residues: 1-1255 c xAna A; Cross-references: 1-1255 c xAna A; Cross-references: GB:XO3363; NID: 931197; PIDN: CAA27060.1; PID: 931198 R; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. R; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. A; Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. A; Title: A v-crbB-ralated protoconcogene, c-crbB-2, is distinct from the c-erbB-1/epiderm A; Reference number: A25491; MUID: 86016729; PMID: 2995967

A; Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P. Science 230, 1131-1139; 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A;Reference number: A44188; MUID:86070181; PMID:2999974

A; Status: translated from GB/EMBL/DDBJ

A, Molecule type: DNA
A, Residues: 832-909 <REX.
A, Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
A, Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R, Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A, Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A, Reference number: I57622; MUID:87286898; PMID:3039351

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA

A; Residues: 1-191 <TAL>

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p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Jease
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa, A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Accession: 148161
A;Accession: 148161
A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
A;Gentics:
A;Gene: neu
C;Genetics:
A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;718-983/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200
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                                                                                                                                                                                                                                                                                                                                                                                                  841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                       PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG
                                                                                                 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAVVMAGVGSP
                                                                                                                                                                                                                                                                                                   781 YVSRLIGICHTSTYQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                                                                                                                                                                                                                                                                                                                                                        LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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86.0%; Pred. No. 8.6e-232;
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Matches 1079; Conservative
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       A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Gomment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Gometics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120633; OMIM:164870
A;Map position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Function:
C;Superfamily: epidermal growth factor receptor; protein; phosphorotein; phosphorotein; phosphorotein; phosphorotein; phosphorotein as a growth factor receptor; protein; phosphorotein; phosphorotein; phosphorotein; protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-553/Domain: signal sequence #status predicted <EXT>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: EGF receptor extracellular domain repeat <EEE>
F;22-1255/Domain: EGF receptor extracellular domain repeat <EEE>
F;24-675/Domain: EGF receptor extracellular domain repeat <EEE>
F;24-675/Domain: EGF receptor extracellular domain repeat <EEE>
F;24-675/Domain: protein kinase homology <KIN>
F;39-605/Domain: protein kinase ATP-binding motif
F;68-124,887,229,530-571,629/Binding site: carbohydrate (ABN)
F;76-734/Region: protein kinase ATP-binding site: carbohydrate (ABN)
F;76-734/Region: protein kinase ATP-binding site: carbohydrate (ABN)
F;76-734/Region: protein kinase ATP-binding site: carbohydrate (ABN)
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F;75-734/Region: protein kinase ATP-binding site: p
Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
Comment: Amplification and overexpression of this erbB-related gene occurs in about
Genetics:
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Pred. No. 1.3e-263;
6; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.6%;
Matches 1225; Conservative
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number: A00641; MUID:84219729; PMID:6328312
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                                                                                                                                                                                                                                                                                                                                                                    ELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVG 783
                                                                                                                                                                                                                                                                                                                                                                                                            SPYVSRLIGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLED 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC 958
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                                                                                                                                          604 RCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATV
                                                                                                                         VPWDQLFRQYIKANSKFIGITELE-CVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                                                                                                                                  ECVEECRVLOGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVA
                                                                                                                                                                                               VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRR
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             TELEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
                             364 NVQEFDGCKKIFGSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYISAWPDSL
                                                                   PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
                                                                                 424 RDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGLALTHRNAHLCFVHT
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A; Residues: 1-29 - (HAL)
A; Residues: 1-29 - (HAL)
A; Cross-references: GB: M38425; NID: g181977; PIDN: AAA63171.1; PID: g553271
A; Experimental source: carcinoma cell line A431-7
R; Xu, Y:; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Nature 399, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is homologous to a v A; Reference number: A00642; MUID: 84245835; PMID: 6330563
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| Db   602 ENNTL-VWKYADAGHYCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGMYGALLLLL 658   Det, C.J.   | KHRSSSTRSGGGDLTLGLEBEEE<br> SP<br> SP<br>   | : :   | Qy         1200 QGGAAPQPHPPPARSPADDLYYWDQDPPERGAPPSTFKGTPTA 1243           Db         1143 QPTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-TA 1192           Qy         1244 ENPEYL 1249           Db         1193 ENAEYL 1193 | RESULT 5 A53183 epidermal growth factor receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 18-Jun-1999 C;Accession: A53183; A43318; A54942; A28941; 845325; I49543 R;Instreke N C: Phillins H K: Oin, T H: Coneland N.G.: Barn, H.S.: Jenkins | Genes Dev. 8, 399-413, 1394 A,Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor A,Reference number: A53133, WUID:94170986; PMID:8125255 A,Accession: A53183 A:Molecule type: mRNA | A; Residues: 1-1210 - LUE> A; Cross-references: GB:U03425 R; Avivi, A; Lax, I; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. | A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding A;Reference number: A43818; MUID:91232866; PMID:2030916 A;Accession: A43818 | A; Molecule Type: mknA<br>A; Residues: 1-714 (AVI><br>A; Cross-references: GB:X59698<br>R; Eisinger, D.P.; Serrero, G. | submitted to the EMBL Data Library, June 1992 A;Reference number: S24942 A;Accession: S24942                    |
|---|---|---|---|---|--|--|--|--|---|
| the EGF receptor (and other tyrosine kinases) can nick double-stranded W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; 9, 33-43, 1989  Le: Functional independence of the epidermal growth factor receptor from srence number: A3331; MUID: 9000323; PMID: 2790560  ment: Binding of EGF to the receptor leads to internalization of the EGF-etics:  GDB: EGFR  Sereferences: GDB: 120610; OMIM: 131550  Bosition: 7p12.3-7p12.1  Serfamily: epidermal growth factor receptor; protein kinase homology ovords: ATP; autophosphory/lation; duplication; glycoprotein; phosphoprotein signal sequence #status predicted <sig> ATP; autophosphory/lation; duplication; glycoprotein; phosphoprotein/s/Domain: EGF receptor astatus predicted <amt> A5/Domain: EGF receptor extracellular domain repeat <eei> 600/Domain: EGF receptor extracellular domain repeat <eei> 668/Domain: EGF receptor extracellular domain repeat <eei> 710/Domain: EGF receptor extracellular domain repeat <eei> 710/Domain: protein kinase ATP-binding motif  110/Domain: protein kinase ATP-binding motif  1110/Region: inhibitory  1110/Region: inhibitory  1110/Region: inhibitory  1110/Region: inhibitory  1110/Region: carbohydrate (ABN) (covalent) #sta</eei></eei></eei></eei></amt></sig> | /45/Active site: Lys #status experimental<br>Query Match<br>Best Local Similarity 49.7%; Pred. No. 2.2e-120;<br>Matches 629; Conservative 174; Mismatches 355; Indels 108; Gaps | Oy 11 LILALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYGGCQVVQGNLELTYLPTN 68 | 129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR  127ANKTGLKELPWRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNH  189 SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP                                | Qy 248 KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD 307 :   | 367 CKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFTLEEITGYLYISAWFDSLFDISVFQ 167 CKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFTLEEITGYLYISAWFDSLFDLSVFQ 1862 CTSISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDLHAFE                    | OY 427 NLQVIRGRILHNGAYSLTLQGLGISWLGLRSIRELGSGLALIHHNTHLCFVHTVPWDQLF 486  | Qy 487 RQYIKANSKFIGITELECVGEGLACHQLCARCHCWGPGPTQCVNCSQPLRGQECVEECRV 546  | QY 547 LQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKP 606  | Qy         607 DLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILL 663           ::::  ::  ::  ::  ::  :: |

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Rilax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstrand. Cell. Biol. 8, 1970-1978, 1988
Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mov
A;Reference number: A27720; MUID:88261272; PMID:3260329
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epidermal growth factor receptor precursor - chicken
NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
NyContains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Species: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
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A/Rochecture (17ge: mRNB. 1116, 70, 4815)

A/Rochecture (17ge: mRNB. 122608

B/Residues: 969-971, 74

A/Rochecture (17ge: mRNB. 122608

B/Hilsermann, G.J.; Gill, G.N.

J. Biol. Chem. 263, 1362-13182 1988

A/Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in A/Rochecture (17ge)

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;1197/Binding site: phosphate (Tyr) (covalent) #status experimental
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45.4%; Score 3087; DB 2; Best Local Similarity 49.5%; Pred. No. 5.5e-119; Matches 630; Conservative 168; Mismatches 363;
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Epidermal growth factor receptor, HER4 - human
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|||::|:|||||||: ||||| || ECVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHFIDGPH 600
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                                                                                      CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
                                                                                                                                                                                                     SAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                                                                                                                                                                                      LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKI PVAIKVLRENTSPKANKEILDEAYVM
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDD
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     A./Molecule type: MRNA
A.Residues: 1.1223 (LAX>
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A.Residues: 1.1223 (LAX>
A.Cross-reference: GB:M20386
R.Milsen, T.W.; Maroney, D.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. Call 41, 719-746, 1985
R.Milsen, T.W.; Maroney, D.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. Call 41, 719-746, 1985
A.Fittle: -c-erbB activation in ALV-induced erythroblascosis: novel RNA processing and protein A.Residues: 585-1223 (MID: 8528222; PMID: 2988784
A.Roteule type: MRNA
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Best Local Similarity 48.5%; Pred. No. 1.8e-118;
Matches 629; Conservative 173; Mismatches 349;
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7.1.112) mrk-Y precursor - southern platyfish transforming wowth factor receptor homolog; kinase-related transforming us (southern platyfish) revision 10-Sep-1999 #text_change 18-Feb-2000
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ID:91125882; PMID:1846957
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h factor receptor; protein kinase homology
receptor; phosphorransferase; transmembrane protein; tyrol
#status predicted <SIG>
ted transforming protein (Tu) #status predicted <MAT>
se homology <KIN>
se ATP-binding motif
------PLAP-SEGAGSDVFDGDLGMGAA 1095
                                                                                                          YSEDPTVPLPS-----ETDGYVAPLTCSPOPEYVNOPDVRPQ 1148
                                                                                                                                                                                                            ATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPH 1208
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|------KNGDLQ------ALDNPEYHNASNG----- 1194
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$; Pred. No. 1.7e-101;
166; Mismatches 391; Indels 140; Gaps
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9; NID:g65284; PIDN:CAA39763.1; PID:g65285
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                                                           QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298
                                                                                                   CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358
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                                240 HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKE
                                                                                                               ITEL-EFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPD
                                                                                                                                                      STNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLMNLTTVKEITGYLVIMMPE
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                     ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLIRIVCAGGC-ARCKGPLPTDCCHE
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A, Esserides 1-1339 (HEL)
A, Cross-references GB.129339; NID:9915389; PID:9915390
A, Experimental source: liver
A, Mote: The authors translated the codon AAC for residue 369 as Thr and GTT for residue
C; Comment: This protein is a functional heregulin receptor that transduces signals to th
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 number: JC4387; MUID:96096535; PMID:8522190
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| QSFQAV 754 Db 60 GPDHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP | Qy 638 DDKGCPAEQFASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL | Qy 697 VEPLTPSGAMFNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR | Qy 757 ENTSPRANKEILDEAYWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR<br>   | Qy   B17 IGSQDLIANMCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE<br> | Qy 877 YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE | 1099 QY 937<br>1077 Db 413 | Qy 996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSTRSG | 1181 Qy 1056 GGDLTLGLEFSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ | Qy         1111 RYSEDPTVPLPSET DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE | Qy         1169 RAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPAF 1213           : :   : :   : :   : :   | 3.; Raines, M  | 1, PID:g211750<br>gnated as Gallus gal   | logy<br>tyrosine-specific p  | ٨  | Gaps 18;  |
|---|---|---|--|--|---|----------------------------|--|--|---|---|--|--|--|--|---|
| NKVLARI FKETELRKLKVLGSGVFGTVHKGIWI PEGESIKI PVCIKVI EDKSGRQSFQAV            | LDEAYVMAGVGSPYVSRLLGICLTSTŸOLVTOLMPYGCLLDHVRENRGRLGSQDLLNWCM<br>    | QIAKGMSYLEDVKLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIK<br>    | WMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPI<br>        <br>WMALESIHFGKYTHQSDVWSYGVTVWELMTFGAEPYAGLRLAEIPDLLEKGERLAQPQI | TIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRS               | LLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSE :      | EBGSDVFDGDLGMGAAKGLQ       | SLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEY :                         | 1140 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSP-GKNGVV :                   | KDVFAFGGAVENPEYLTPQGGAAPQPHPP 1210<br>                                      | RESULT 11 TUFVLV TUFVLV Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine C;Species: avian leukosis virus, ALV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999 C;Accession: BO6443. | Cjaccession: BU0643; BU0643<br>R;Nilsen, T.W.; Marconey, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittende<br>Cell 41, 719-726, 1985<br>A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA<br>A;Reference number: A00643; MUID:85228222; PMID:2988784 | A;Molecule type: mRNA<br>A;Residues: 1-698 ANL.<br>A;Cross.references: GB:M10066; GB:M13881; NID:g211749; PIDN:AAA48763.1; PII<br>A;Note: in Genbank entry CHKERBBF, release 109.0, the source is designated | <pre>v-erbB' epidermal growth factor receptor; protein kinase homology ?; oncogene; phosphotransferase; transforming protein; tyrosine</pre> | F;1-6/Product: gag protein (fragment) #status predicted <gag> F;1-5/Product: env protein (fragment) #status predicted <env> F;60-69/Product: protein-tyrosine kinase erbB #status predicted <eri <kin="" domain:="" f;194-459="" homology="" kinase="" protein=""> F;202-210/Region: protein kinase ATP-binding motif F;229/Active site: Lys #status predicted</eri></env></gag> | 26.0%; Score 1766.5; DB 1; Length 698; ty 52.2%; Pred. No. 2.5e-65; ervative .80; Mismatches 137; Indels 125; |

Tue

transforming protein; tyrosine-specific

Keywords: ATP; oncogene; phosphotransferase;

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1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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                                                                                                                                                         647 RASPLISIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLIPSGA 705
                                                                                                                              CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP--- 58
                                                                                                                                                                      NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                          298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKYYDGIPASEISSVLEKGERLPQPP
                                                                                                                                                                                                                                                          EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                             Indels 126;
                                                    Length 604;
                                                    25.0%; Score 1703; DB 1; 1
52.2%; Pred. No. 8.5e-63;
iive 76; Mismatches 128;
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Best Local Similarity 52.24
Matches 360; Conservative
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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: avian erythroblastosis virus C;Species: 33-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C;Accession: S35745
R;Vennstroem, B.
submitted to the EMBL Data Library, March 1993
A;Rcession: S35745
A;Molecule type: DNA
A;Residues: 41-544 <VEN>
A;Residues: 41-544 <VEN>
A;Cession: S35745
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:
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996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
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                                                                                              GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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                                                                                                                                            DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                      Gaps
                                                                     92;
                                                                      Indels
                                                Length
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                                                          Best Local Similarity 54.9
Matches 345; Conservative
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% National Common and the state of mutation in the erbB (EC 2.7.1.-) - avian erythroblastosis virus (% Natase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus (% Species: avian erythroblastosis virus (% Species: avian erythroblastosis virus (% Species: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 28-Feb-1997 (%) Accession: 80727 (%) 1987

Genetics:
A;Gene: erbB
A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: phosphotransferase
C;Keywords: ATP; phosphotransferase
F;135-400/Domain: protein kinase homology <KIN>

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Best Local Sim
Matches 340;
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By 4776

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)
C; Species: avian erythroblastosis virus
C; Species: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 04-Feb-2000
C; Accession: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 04-Feb-2000
C; Accession: 28-Apr-1990
R; BIUBKin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzman, R.C.
Oncogene 5, 15-24, 1990
A; Title: Six amino acids from the retroviral gene gag greatly enhance the transforming p, A; Reference number: A44776; MUD:90206603; PMID:1969616
A; Accession: B44776
A; Accession: B44776
A; Reducule type: mRNA
A; Residues: 1-540 < BRU>
A; Canetics:
A; Genetics:
A; Genetics:
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP: phosphotransferase; tyrosine-specific protein kinase
F;130-395/Domain: protein kinase ATP-binding motif
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                                                                                   578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                   DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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                                                        Gaps
                                                       92;
                           Length 545;
                                                       69; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 1640; DB 2; 54.9%; Pred. No. 2.9e-60;
F;143-151/Region: protein kinase ATP-binding motif
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                                                     Matches 345; Conservative
                                          Best Local Similarity
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                                                         14;
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                                                                                                            587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
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                                                         90;
        Length 540;
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                                                         Indels
23.9%; Score 1623; DB 2;
.larity 54.9%; Pred. No. 1.4e-59;
Conservative 69; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SRTPLLSSLSATSNNSATNCIDRNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: July 22, 2003, 09:09:55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SHSTAVDNPEYL 539
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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec

SEQ4-579-593-12 6803 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Perfect score: Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Ø         | Description   | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        | kinase-related tra | protein-tyrosine k | protein-tyrosine k | epidermal growth f | protein let-23 [im | protein-tyrosine k | protein-tyrosine k | epidermal growth f |        | growth | 5      | protein-tyrosine k | insulin-like growt | insulin-like growt | insulin receptor p |
|-----------|---------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | qı            | A24571             | TVRTNU             | 148161            | GQHUE              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV             | TVYUH              | GOFFE              | S35745 | 800727             | B44776             | TVFVEB             | A36325             | E88257             | 870712             | S70713             | A45558             | A42032 | A27131 | S13807 | S13808             | T43220             | 321                | A36080             |
|           | DB            | -                  | Н                  | 7                 | П                  | 7      | П      | 7      | Η,     | ~                  | 7                  | Н                  |                    |                    |        |                    |                    |                    | ~                  |                    |                    |                    |                    | 7      | ~      | ~      | N                  | ~                  | 7                  | 7                  |
|           | Length        | 1255               | 1260               | 1254              | 1210               | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698                | 604                | 1330               | 544    | 545                | 540                | 540                | 644                | 1323               | 1374               | 1369               | 1717               | 527    | 843    | 346    | 311                | 1363               | 0                  | 1383               |
| de        | Query         | 97.8               | 86.1               | 85.9              | 45.8               | 45.4   | 45.0   | œ.     | 38.8   | 35.1               | 33.9               | ů.                 | 24.8               | 24.0               | 23.8   | 23.7               | 23.4               | m.                 | •                  | σ                  | 19.0               |                    | ٠                  | 16.6   | ٠      | 11.9   | 11.1               | 10.6               | •                  | 10.2               |
|           | Score         | 6651               | 5856               | 5846.5            | 3116               | 3089   | ٠.     | 2956.5 | 2641   | 2388.5             | 2304.5             | 1736.5             | 1688               | 1630.5             | 1617   | 1610               | 1593               | 1591               | 1477               | 1294               | 1294               | 1211               | 1176               | $\sim$ | 976.5  |        | 754.5              | 723                | σ                  | 9                  |
|           | Result<br>No. | 7                  | 7                  | e                 | 4                  | Ω.     | φ      | 7      | œ      | σ                  | 10                 | 11                 | 12                 | 13                 | 14     | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 |                    |                    | 23     |        | 25     | 56                 | 27                 |                    | 29                 |

|  | mouse developmenta | protein-tyrosine k | receptor tyrosine | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | insulin receptor - | insulin receptor ( | insulin-like growt | insulin receptor - | insulin-like growt | insulin receptor-r | protein-tyrosine k | insulin receptor p | insulin receptor-r | insulin receptor p |
|--|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| INHUR<br>A36502<br>A34157<br>T34157<br>T36502<br>IGHUR1<br>A3363<br>A3363<br>A3363<br>A39753<br>A39753<br>A39753<br>IS6102<br>IS6102 | 148652             | I50612             | 151672            | 833596             | A39753             | A54092             | T30346             | S57245             | A33837             | A56081             | IGHUR1             | B36502             | T18534             | A34157             | A36502             | INHUR              |
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| 1382<br>1372<br>1372<br>1268<br>1368<br>1371<br>2101<br>1390<br>987<br>987<br>9887   | 987                | 952                | 985               | 1091               | 984                | 987                | 1390               | 2101               | 1371               | 2148               | 1367               | 1268               | 1477               | 1372               | 1300               | 1382               |
| 011100000000000000000000000000000000000  | 8                  | 8.5                | 9.8               | 8.6                | 80                 | ω                  | 9.1                | 9.1                | 9.1                | 9.5                | 9.4                | 9.9                | 10.0               | 10.0               | 10.1               | 10.1               |
| 685.5<br>685.5<br>687.5<br>627.5<br>627.3<br>621.6<br>621.6<br>621.6<br>631.5<br>83.5<br>83.5<br>84.1.5                              | 580                | 581.5              | 583.5             | 586                | 599.5              | 009                | 619                | 621                | 622                | 627.5              | 641                | 673                | 678                | 682.5              | 685.5              | 989                |
| 6 6 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9  | 45                 | 44                 | 43                | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35                 | 34                 | 33                 | 32                 | 31                 | 30                 |

## ALIGNMENTS

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protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB C;Species: Homo sapiens (man) C;Date: 25-Oct-1987 #sequence\_revision 06-Dec-1996 #text channe 11-1000

C;Date: 25-Oct.1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999 C;Accession: A24571; A25491; Ā44188; B44188; I59509; I57622 C;Accession: A24571; A25491; Ā44188; B44188; I59509; I57622 A;Aramanoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Nature 319, 230-234, 1986 A;Yitle: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f A;Reference number: A24571; MUID:86118663; PMID:3003577

A;Accession: A24571

A;MOLecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1255 <YAM> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U. S.A. 82, 6497-6501, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm A;Reference number: A25491; MUID:86016729; PMID:2995967

A; Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

A; cross references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R; Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, B.; Gray, A.; McGrath, J.; Seeburg, P Science 230, 1132-1139, 1985

A;Title: Tyrosine kinase receptor with extensive homology to BGF receptor shares chromose A;Reference number: A44138; MUID:86070181; PMID:2999974

A; Accession: A44188

A;Molecule type: DNA A;Residues: 740-910 <COUL> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A;Residues: 1.517, "MLL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M1730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: I59509; MUID:85272597; PMID:2992089

A; Status: translated from GB/EMBL/DDBJ

A,Molecule type: DNA
A;Residues: 832-909 <REX.>
A;Cross-references: GB:L29395; NID:9459807; PIDN:AAA35809.1; PID:9459808
A;Cross-references: GB:L29395; NID:9459807; PIDN:AAA35809.1; PID:9459808
B;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional A;Reference number: 157622; MUID:87286898; PMID:3039351

A;Accession: 157622 A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 1-191 <TAL>

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protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 EEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                                                                        RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTSPKANKEI LDEAYVMAGVGSP
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           PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG
                                                              ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                                             RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Goment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Goment: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Nap position: 17421.1-17471.1
A;Introne: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Doscription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Kewwords: ATP; autophosphorylation; duplication; glycoprotein; phosphorylation; duplication; glycoprotein; phosphorylation; duplication; glycoprotein; phosphorylation; cxtracellular factor receptor; protein repeat of EED:
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted of EED:
F;22-653/Domain: extracellular founain repeat of EED:
F;22-653/Domain: EGF receptor extracellular domain repeat of EED:
F;24-653/Domain: EGF receptor extracellular domain repeat of EED:
F;395-605/Domain: intracellular #status predicted of TYMM:
F;765-734/Region: protein kinase homology of KIN>
F;76-734/Region: protein kinase predicted of TYMP
F;76-734/Region: protein kinase predicted of TYMP
F;75-73/Active site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F;686/Binding site: phosphate (Thr) (covalent) (covalent) (by autophosphorylation)
F;713/Active site: Lys #status predicted
F;1139,1221,1222,1224/Binding site: phosphate (Tyr) (covalent) (Tyr)
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97.6%; Pred. No. 2.1e-265;
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Matches 1225; Conservative
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C;Species: Mescorricetus auratus (golden hamster)
C;Species: Mescorricetus auratus (golden hamster)
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y
Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Accession: 148161
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                  EGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPPFTDGYVAPLACSPQPE
     EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE
                                                         WMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
                                                                                                                            DAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPS
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A; Residues: 1-1254 aRES>
A; Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1;
C; Genetics:
A; Gene: neu
C; Superfamily: epidermal growth factor receptor; protein kina
C; Superfamily: epidermal growth factor receptor; protein kina
C; Reywords: ATP
F; 718-983/Domain: protein kinase homology aKIN>
F; 726-734/Region: protein kinase ATP-binding motif
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F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covale F;691/Binding site: phosphate (Thr) (covalent) #status predicted F;758/Active site: Lys #status predicted F;882,1227,1253/Binding site: phosphate (Tyr) (covalent)
                                                                                                                                                                          Indels
                                                                                                                                        86.1%; Score 5856; DB 1;
86.0%; Pred. No. 7.9e-233;
                                                                                                                                                                          56; Mismatches 118;
                                                                                                                                                                         Matches 1081; Conservative
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transcript terminat

B.A.; Mer

homologous to a variety of RNAs

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A; Molecule type: mRNA
A; Residues: 1-1210 <ULL>
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
B; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
B; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
A; Title: Characterization and sequence of the promoter region of the human epidermal gro
A; Reference number: A25772; MUID:85270438; PMID:2991899
                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-29 - ISH>
A,Kresidues: 1-29 - ISH>
A,Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification
A;Reference number: S30024; MUID:88217333; PMID:3329716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R; Haley, J.D.; Waterfield, M.D.
J. Baol, Chem. 266, 1746-173, 1991
A; Haley, J.D.; Waterfield, M.D.
A; Haley, J.D.; Waterfield, M.D.
A; Haley, J.D.; Waterfield, M.D.
A; Title: Contributory effects of de Novo transcription and premature transcript A; Reference number: A38672; MUID:91107677; PMID:1988448
A; Reference number: A38672; MUID:91107677; PMID:1988448
A; Residues: 1-29 chAL.
A; Residues: 1-29 chAL.
A; Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A; Cross-reference: carcinoma cell line A431-7
K; Xu, Y; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, Nature 309, 806-810, 1984
number: A00641; MUID:84219729; PMID:6328312
                                                                                                                                                                                                                                                                 A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-29 <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S30024
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                          ELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
                                                                                                                        DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                                                                                                              PWDQLFRNPHQALLHTANR PEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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A; Molecule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195,' M', 197,' A', 199-222,' S', 224-304,' RA', 307-321
', 798-799, 'TD', 802-811,' R', 813-942 < KUY>
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF recep
R; Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.
Science 224, 843-848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplification
A; Reference number: A43615; MUID:84196372; PMID:6336261
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A;Residues: 740-74, YX, 746-747 <RUS>
A;Residues: 740-74, YX, 746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth factor receptor A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Reference number: receptor activity
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A; Mesidues: 713-964 «LIN»
A; Residues: 713-964 «LIN»
A; Experimental source: epidermoid carcinoma cell line A431
R; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter,
Biochem. Blophys. Res. Commun. 124, 125-132, 1984
A; Reference number: A23062; WUID: 85046483; PMID: 6093780
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PMID:2985580
A;Title: Human epidermal growth factor receptor cDNA is A;Reference number: A00642; MUID:84245835; PMID:6330563 A;Accession: A00642
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A; Residues: 1028-1210
R; Weber, W.; Gill, GN.; Speiss, J.
Science 224, 294-297, 1984
A; Reference number: A05281; MUID:84172183; PMID:6324343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A;Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleoti:
A;Reference number: A60143; MUID:85182650; PMID:298:
A;Accession: A60143
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| Db 602 ENNTL-VWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGMVGALLLLLL  Qy 664 VVLGVVFGILIKAROQKIRKYTMRELLQETELVEPLTPSGAMPNQAQMRILKETELRKV   | QY         1023 YLVPQQGFFCPDPAPGAGGWYHHRHRSSTRSGGGLTLGLEPSEEAPRSPLAPSEGAG 1082           Db         1016 YLIPQQGFF           1016 YLIPQQGFF  | RESULT 5 A53183 epidermal growth factor receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: (6-Jan-1995 #text_change 18-Jun-1999 C;Accession: A53183; A43818; S24942; A28941; S45325; I495643 C;Accession: A53183; A43818; E324942; A28941; S45325; I495643 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A. Genes Dev. 8, 399-413, 1594 A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor A;Reference number: A53183 A;Accession: A53183 A;Accession: A53183 A;Accession: A25183 A;Accession: A43818 A;Accession: A43818 A;Accession: A43818 A;Accession: A43818 A;Accession: A43818 A;Accession: A43818 A;Reference number: A3888; MUID:91232866; PMID:2030916 A;Residues: 1-114 <ani>A;Residues: 1-114 <ani>A;Residues: B. Serior Comparation of EGF receptor sequences as a guide to study the ligand binding shallesinger, D.b.; Serior ERRS A;Accession: A43818 A;Accession: A43818 A;Residues: 1-14 <ani>A;Residues: 1-15 <ali <ani="">A;Residues: 1-15 <ali 1-15="" <a<="" <ali="" <ani="" a;residues:="" th=""></ali></ali></ani></ani></ani> |
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| tinases) can nick double-stranded DNA J.B.; Chang, C.P.; Walton, G.M.; Der, mal growth factor receptor from a doma tD:2790960  Is to internalization of the EGF-recept ion; glycoprotein; phosphoprotein; pho- ted <sig> red <amt> ed <sig> comain repeat <ee1> comain repeat <ee2> ted <aty> comain repeat <ae2> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn> ted <tymn <tymn="" td="" ted="" ted<=""><td>Query Match  45.8%; Score 3116; DB 1; Length 1210;  Best Local Similarity 49.6%; Pred. No. 1.36-120;  Matches 628; Conservative 174; Mismatches 356; Indels 108; Gaps  11 LLALLPPGAASTQCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN                                       </td><td>  QY   248   KHSDCLACLHFNHSGTCELHCPALVTYNTDTFESMRNPEGRYTFGASCYTACPYNYLSTD 307   244   RESDCLACLHFNHSGTCELHCPALVTYNTDTFESMRNPEGRYTFGASCYTACPYNYLSTD 303   244   RESDCLYCRKFDEATCKGTCPPLMLYNTTYNDWDVPEGRYFGGATCKCFRNYVYDD 303   308   VGSCTLVCPLHNGEVTAEDGTQRCEKCSKCRCACGLGMQYIKANSKFIGITELE-PAG 366                                    </td></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></tymn></ae2></aty></ee2></ee1></sig></amt></sig> | Query Match  45.8%; Score 3116; DB 1; Length 1210;  Best Local Similarity 49.6%; Pred. No. 1.36-120;  Matches 628; Conservative 174; Mismatches 356; Indels 108; Gaps  11 LLALLPPGAASTQCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN | QY   248   KHSDCLACLHFNHSGTCELHCPALVTYNTDTFESMRNPEGRYTFGASCYTACPYNYLSTD 307   244   RESDCLACLHFNHSGTCELHCPALVTYNTDTFESMRNPEGRYTFGASCYTACPYNYLSTD 303   244   RESDCLYCRKFDEATCKGTCPPLMLYNTTYNDWDVPEGRYFGGATCKCFRNYVYDD 303   308   VGSCTLVCPLHNGEVTAEDGTQRCEKCSKCRCACGLGMQYIKANSKFIGITELE-PAG 366   |

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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallub gallus (chicken)
C;Dacess: Gallub gallus (chicken)
C;Accession: A27720; A00643
R;Lax, I: Johnson, A: Howk, R: Sap, J:; Bellot, F:; Winkler, M.; Ullrich, A.; Vennstr Mol. Cell. Biol. 8; 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mou A;Reference number: A27720; MUID:88261272; PMID:3260329
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                      SVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRBLGSGLALIHHNTHLCFVHTVPW
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A, Molecule type: mRNA
A, Residues 169-97. Y. (%) 973-1115, D' < EIS>
A, Cresidues 169-97. Y. (%) 973-1115, D' < EIS>
A, Cresidues 169-97. Y. (%) 973-1115, D' < EIS>
A, Cresidues 169-97. Y. (%) 973-1115, D' < EIS>
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A, Accession: A2894; MID: 84325
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A, Accession: Accession of the epidemal growth factor receptor; protein kinase homology
C, Accession: May 5443
A, Accession: May 5443
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A, Accession: Accession of the epidemal growth factor receptor; protein kinase homology
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                 ECVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHFIDGPH 600
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                                                                                                   CVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
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                                                                                                                                                                                                          656 SAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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A;Accession: %27720
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A;Residues: 1-123 claX>
A;Cross-references: GB:M20386
R;Milsen, T. W; Macroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
R;Alisen, T. W; Macroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
R;Alisen, T. W; Macroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
R;Reference number: A00643; MUID:85228222; PMID:2988784
A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Residues: 585-1233 cMIL>
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C;Keywords: alternative splicing; AFP; autophosphorylation; glycoprotein; growth factor receptor & Etator
C;Keywords: alternative splicing; AFP; autophosphorylation; glycoprotein; growth factor
C;Keywords: alternative splicing; AFP; autophosphorylation; glycoprotein; growth factor
C;Keywords: alternative splicing AFP; autophosphorylation; glycoprotein; growth factor
C;Keywords: alternative splicing after spredicted cSTS>
F;1-100/Domain: expreceptor extracellular domain repeat cEE2>
F;1-100/Domain: extracellular #status predicted cSTS>
F;1-100/Domain: Extracellular #status predicted cINT>
F;7-7735/Region: protein kinase homology cKIN>
F;7-7735/Region: protein kinase homology cKIN>
F;719-984/Domain: intracellular #status predicted cINT>
F;719-984/Domain: intracellular #status predicted cINT>
F;719-984/Domain: intracellular domain speaker (EE2>
F;199,650/Bainding site: carbohydrate (Ger) (covalent) #status predicted
F;136,720;280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;100/Illa3,1208/Binding site: phosphate (Tyr) (covalent) (by protein kinase C) #status predicted
F;100/Illa3,1208/Binding site: phosphate (Tyr) (covalent) (by autophorylation) #status
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| 28  | 64 | 67                       | 124  | 184 | 178  | 243  | 237                           | 0   | 297 | 363   |                          | 415 | 483  | 475 | 543  | 535   | 602  | LO. | 652  | 710   | 708                                | 770 | 768 | 830 | 828  | 890 | 888   | 95  | σ,              | 100  |      |
| 43.5%; Score 2956.5; DB 2; Length 1308;<br>Similarity 45.2%; Pred. No. 4.7e-114;<br>9; Conservative 181; Mismatches 383; Indels 173; Gaps |    | WWWSLLVAAGTVQPSDSQSVCAGT | LPTNASLSFLØDIOEVGGYVLIAHNQVROVPLØRLRIVRGTØLFEDNYALAVLDNGDPLN |     |      | DINRSRACHPCSPWCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG | STNGSSGCGRCHKSCTG-RCWGPTENHCQ | CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYN | -   | LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE  - | FAGCKK1 FGST.AFT. DESFED | —ı  | VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHN |     | QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE | TESTINGRIVIRDNRKAENCTAEGMVCHHLCSSDGCWGPGPDQCL | CRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPBADQCVACAHYKDPPFCVARCPQ     .   .   .   .   .   .   .   . |     | :: : | TSIVSAVV-GILLVVVLGVVPGILIKRRQKIRKYTMRRLLQBTELVEPLTPSGAMPNQA | IAAGVIGGLFILVIVGLTFAVYVRKKSIK-KKRA | -   | _   |     | ALIMASMDHPHLVRLÍGYCĽSPTIQĽVTQLMPHGCĽLEYVHEHKDNIGSQLLLMWCVQIA |     | I KGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLLEGDEKEYNADGGKMPIKWMA | LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI |                 | VYMIMVKGMAIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LGFASPLDSTFYRSLL<br> |      |
| itch<br>ial<br>60   | 9/ | α0                       | 6 6  | 125 | 128  | 185  | 179                           | 244   | 238 | 304   | 364                      | 356 | 424  | 416 | 484  | 476   | 544  | 603 | 596  | 652   | 653                                | 711 | 709 | 171 | 769  | 831 | 829   | 891   | 66.<br>88<br>88 | 951  | 1016 |
| Query Ma<br>Best Loc<br>Matches   | ò  | Dp                       | <u>کن</u> و  | à   | e qo | ò  | qq                            | کن<br>ان  | മ   | <u>ک</u> ج  | : è                      | ; A | ò  | qq  | ò  | q <sub>Q</sub>                                | رم<br>م  | ò   | · අ  | ò   | QQ<br>Q                            | ò   | дg  | ò   | QQ   | ò   | a<br>a  | ð í   | a<br>a          | `<br>& &   | 3 &  |

Tu loci A; Accession: S00142
A; Molecule type: DNA
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A; Molecule: 1-1166 (wIT>
A; Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
B; Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A; Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophoru:
A; Reference number: S13807; MUID:91125882; PMID:1846957
A; Accession: S13809
A; Status: preliminary; translation not shown
A; Molecule type: DNA
A; Residues: B21-1025, N', 1027-1098, A', 1100-1166 (ADA>
A; Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
C; Genetics: A, Map position: Y
A, Introns: 872/3; 888/1; 947/1; 979/3; 1025/3; 1056/1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; tyro:
C; Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; tyro:
E;1-25/Domain: signal sequence #status predicted <SIG>
E;25-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
E;707-972/Domain: protein kinase Amp-binding motif A.; Roberts transforming melanoma-inducing 1116 1167 1237 ENPFVSRR------PPKAE 1199 1200 DEYVNEPLYLNTFANTLGKAEYLKANILSMPEKAKKÁFDNPDÝWNHSLPPRSTLQHPDYL 1259 101 LPTHDPSPLQRYSEDPTVPLPS-----ETDGYVAPLICSPQPEYVNQPDVRPQPPSPR 1153 30; 119 120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 59 62 Dioctein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish NyAlternate names: epidermal growth factor receptor homolog; kinase-related to cypecies: Xphophorus maculatus (southern platyfish)
C;ppecies: Xphophorus maculatus (southern platyfish)
C;pate: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Feb-2000
C;Accession: S06142; S13809
R;Witchrodt, J; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989
Nature 341, 415-421, 1989
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-indi A;Reference number: S06142; MUID:90015140; PMID:2797166 -- PLAP - SEGAGSDVFDGDLGMGAAKGLQS 1117 PHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE------------PPSTF 8 AALLQ.--LLLVLSISRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKAMYSGCNVVLEN LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 4 AALCRWGLLLALLPPGAAST----QVCTGTDMXLRLPASPETHLDMLRHLYQGCQVVQGN EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA-Indels 140; Length 1166; 38.8%; Score 2641; DB 1; llarity 44.9%; Pred. No. 3.5e-101; Conservative 167; Mismatches 392; 1260 QEYSTKYFYKQNGRIRPIVAENPEYL 1285 Best\_Local Similarity Matches 569; Conserv KGTPT---1070 APRS 9 1009 1168 1238 1154 1213 Query Match 염 셤 ò 셤 g ò q ò g q ⋩ ò ò ò ò

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  of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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                                                                                                                                                                                                                                                            AGSDVPDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                   IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; cancer; prostate cancer; ovarian cancer; lung cancer;
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                                                                                                                                                                                                                                                                                                                                        The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polymuclectide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an erbB 2 receptor protein designated SPLICE the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the SPLICE erbB-2 receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated prepared HERZ/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (TLL) that is culture in vitro and binds to a complex of an epitope (I), bound to a num a second epitope antigen (HLA) molecule: (2) a peptide (II) comprising (I) and a second epitope antigen (HLA) molecule: (2) a peptide (II) comprising (I) and as second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HERZ/neu; (3) a vaccine composition (III) comprising (II) and (5) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (1) has cytostatic and immunosimulates, and can be used in vaccines (I), (II) and (III) are useful for the prevention and treatment of cancer. (I) and (II) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple tumour-associated molecules addressing the problem of tumour-accines provides the opportunity to combine epitopes darived from the same pathogen. Epitope-based anti-tumour-accined formulation and pathogen in the pathogen of tumour-accined to multiple tumour-associated molecules addressing the problem of tumour-accined to multiple tumour-associated molecules addressing the problem of tumour-accined to multiple tumour-accined the ability to direct and focus an immune of tumour-accined to antigent and accined provides the ability to direct and focus an immune of fumour-accined provides the ability to direct and focus an immune 
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cancer -
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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                                                                                                                                NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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1140

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960 960

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840 900 900

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

July 22, 2003, 08:25:54; Search time 22.9062 Seconds (without alignments) 5267.077 Million cell updates/sec Run on:

SEQ4-369-383-12

68Î5 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | protein-tyrosine k | protein-tyrosine k | p-185 precursor - | epidermal growth f |        |        |        | >      | kinase-related tra | epidermal growth f |        | protein-tyrosine k | protein-tyrosine k | -      |        |        | growth | epidermal growth f | et-23 [i | protein-tyrosine k | yrosine |        |        |        | >      |        | insulin-like growt | insulin receptor p |        |
|-----------|-----------------------|--------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|--------------------|----------|--------------------|---------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|
| SUMMARIES | ID                    | A24571             | TVRTNU             | 148161            | СОНОЕ              | A53183 | TVCHLV | A47253 | S06142 | A36223             | JC4387             | TVFVLV | TVYUH              | S35745             | S00727 | B44776 | TVFVEB | GQFFE  | A36325             | E88257   | 870712             | S70713  | A45558 | A42032 | A27131 | S13807 | S13808 | T43220             | INHUR              | A36080 |
|           | DB                    | 7                  | ٦                  | ~                 | Н                  | ~      | Н      | 7      | -      | ~                  | N                  | -      | ч                  | ~                  | 7      | 7      | 7      | ٦      | ~                  | 7        | 7                  | 7       | Н      | 0      | ~      | ~      | ~      | 7                  | Н                  | 7      |
|           | Query<br>Match Length | 1255               | 1260               | 1254              | 1210               | 1210   | 1223   | 1308   | 1166   | 1342               | 1339               | 698    | 604                | 544                | 545    | 540    | 540    | 1330   | 644                | 1323     | 1374               | 1369    | 1717   | 527    | 843    | 346    | 311    | 1363               | 1382               | 1383   |
| di        | Query                 | 97.6               | 9                  | 85.9              | 45.4               | S      | 4      | 42.8   | 38.7   | 34.7               | 33.5               | 25.9   | 25.0               | 24.2               | 24.1   | 23.8   | 23.8   | 23.5   | 21.4               | 18.7     | 18.7               | 17.5    | 17.0   | 15.9   | 13.9   | 11.8   | 11.1   | 10.7               | 10.2               | 10.2   |
|           | Score                 | 6653               | 5859               | 5851.5            | 3097               | 3069   | 3052.5 | 2919.5 | 2636   | 2366.5             | 2280.5             | 1766.5 | 1703               | 1647               | 1640   | 1623   | 1621   | 1600.5 | 1461               | 1275     | 1275               | 1192    | 1161   | 1084   | 945.5  | 806.5  | 754.5  | 730                | 697                | 969    |
|           | Result<br>No.         | ,<br>,             | 7                  | m                 | 4                  | 2      | 9      | 7      | 89     | თ                  | 10                 | 11     | 12                 | 13                 | 14     | 15     | 16     | 17     | 18                 | 19       | 20                 | 21      | 22     |        |        |        |        |                    | 28                 | 29     |

| insulin-like growt | insulin receptor p | protein-tyrosine k | insulin receptor-r | insulin receptor-r | insulin-like growt | insulin receptor - | insulin-like growt | insulin receptor - | insulin receptor ( | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | protein-tyrosine k | tyrosine kinase Mp |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T43212             | A34157             | T18534             | A36502             | B36502             | IGHUR1             | T30346             | A33837             | A56081             | S57245             | A54092             | S05582             | A39753             | 833596             | I50612             | S49004             |
| 7                  | N                  | 7                  | N                  | 7                  | П                  | 0                  | 7                  | Н                  | N                  | N                  | ٦                  | 0                  | 7                  | 0                  | ~                  |
| 1607               | 1372               | 1477               | 1300               | 1268               | 1367               | 1390               | 1371               | 2148               | 2101               | 987                | 1114               | 984                | 1091               | 952                | 716                |
| 10.2               | 10.2               | 6.6                | 9.9                | 9.7                | 9.4                | 9.5                | 9.5                | 0.6                | 0.6                | 8.8                | 9.8                | 8.6                | 9.6                | 9.8                | 8.5                |
| 969                | 695.5              | 929                | 673.5              | 664                | 644                | 627                | 625                | 615.5              | 612                | 599                | 588                | 587.5              | 586                | 585.5              | 581.5              |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

#### ALIGNMENTS

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protein-tyxosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erb\_Cspecies: Homo sapiens (man) c;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; IS9509; IS7622 Namonto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Nature 319, 230-234, 1986 #totein encoded by the human c-erb-B-2 gene to epidermal growth the A;Reference number: A24571; MUID:86118663; PMID:3003577

A, Accession: A24571
A, Molecule type: mRNA
A, Residues: 1-1255 < YAM>
A, Residues: GB:X0<u>1</u>363; NID:g<u>3</u>1197; PIDN:CAA27060.1; PID:g31198

RiSemba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985.
A;Title. A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidern A;Reference number: A25491; MUID:86016729; MID:2995967

A; Accession: A25491

A; Molecule type: DNA
A; Residues: 737-1031 <SEM>
A; Residues: 737-1031 <SEM>
A; Residues: 737-1031 <SEM>
A; Residues: 737-1031 <SEM>
A; Cross-references: GB: MID: g182163; PIDN: AAA35808.1; PID: g553282
B; Crossens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, B.; Gray, A.; McGrath, J.; Seeburg, F Science 230, 1132-1139, 1985
A; Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos A; Reference number: A44188; MUID: 86070181; PMID: 2999974

A;Molecule type: DNA A;Residues: 740-910 <COU1> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A;Molecule type: mRNA A;Residues: 1-517, RALL', 522,'S',524-654,'V',656-1169,'A',1171-1255 <COUZ> A;Cross-references: GB:M11730; NID:g183986 K;King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985 A;Title: Amplification of a novel V-erbB-related gene in a human mammary carcinoma. A;Reference number: I59509; MUID:85272597; PMID:2992089

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 832-909 <REXA;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
A;Reference number: 157622; MUID:87286898; PMID:3039351

A; Status: translated from GB/EMBL/DDBJA; Molecule type: DNA

A; Residues: 1-191 <TAL>

```
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1.1260 - CBMBL: No.362; NID:956745; PIDN:CAA27059.1; PID:956746
R;Macule type: mRNA
A;Residues: 1.1260 - CBMBL: NID:956745; PIDN:CAA27059.1; PID:956746
R;Maculi, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no n A;Reference number: A61204; MUID:92035293; PMID:1682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: neu S. Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphocyfaction; duplication; glycoprotein; phosphoprotein; phosphore; F;1-19/Domain: signal sequence #status predicted <SIGS F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                             YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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                                                                                                                                                                                         RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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A;Motecule type: DNA
A;Residues: 637-663, VV,665-702 <MAS>
A;Note: authors translated the codon GCA for residue 25
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A;Cross-references: GB:Mi6792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
C;Genetics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 1721.1-1720613;
A;Note: the list of introns is incomplete
C;Function:
A;Note: the list of introns is incomplete
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: AFP; autophosphorylation; duplication; glycoprotein; phosphorylation; diplication; glycoprotein; phosphorylation; duplication; glycoprotein; phosphorylation; diplication; glycoprotein; phosphorylation; extracellular domain repeat centracellular factors centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain repeat centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain repeat centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracellular domain centracel
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97.6%; Score 6653; DB 1;
Best Local Similarity 97.6%; Pred. No. 6.5e-265;
Matches 1225; Conservative 8; Mismatches 22;
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p-18b precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; I
Gene 140, 251-255, 1994
A;Title: (Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: 148161; MUID:94193007; PMID:7908275
A;Accession: 148161
A;Accession: 148161
A;Accession: 148161
A;Accession: 148161
A;Residues: 1-1254 cRES>
C;Genetics:
A;Gene: neu
C;Genetics:
A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATR-983/Domain: protein kinase homology c;T18-983/Domain: protein kinase ATP-binding motif
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                                                     WMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
                                                                                                                      DAEEYLVPQQ3FFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPS
                                                                                                                                                      DAEEYLVPQQ3FFSPDPTPGTGSTAHRRHRSSTRSGGGELTLGLEPSEEGPPRSPLAPS
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                   FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
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Pred. No. 3.7e-232;
64; Mismatches 115;
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/718-983/Domain: protein kinase homology <KIN>
/726-734/Region: protein kinase ATP-binding motif
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Best Local Similarity 85.7%;
Matches 1075; Conservative 6.
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                                                      (covalent) #status
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F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-984 Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263;535,576,634/Binding site: carbohydrate (Asn) (covales F;691/Binding site: phosphate (Thr) (covalent) #status predicted F;758/Active site: Lys #status predicted F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status
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86.0%; Pred. No. 1.8e-232;
iive 54; Mismatches 120;
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Best Local Similarity 86.09
Matches 1081; Conservative
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A; Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
B; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe B.A.; Merlino, G.T.; Pastan, I.
Proc. NaL1. Acad. Scil. US.A. 82, 4920-4924, 1985
A; Reference number: A25772; MUID:85270438; PMID:2991899
A; Reference number: A25772
A; Received type: DNA
A; Residues: 1-29 cISH
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A/Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321'
A/Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321'
A/RESPECTIMENTED SOURCE: A431 human carcinoma cells, which have large numbers of EGF reception, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.S.; Mererseaton cloning of human EGF receptor complementary DNA: gene amplification A/Reference number: A43615 MUID:84196372; PMID:6326261
A/Rocession: A43615
A/Rocession: A43615
A/Rocession: A43615
A/Rocession: A2362
A/Rocession: Biophys. Res Commun. 124, 125-132, 1984
A/Reference number: A23062; MUID:85046483; PMID:6093780
A/Rocession: A23062
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A, Residues: 1-29 - (HA2>
A, Residues: 1-29 - (HA2>
A, Residues: 1-29 - (HA2>
A, Across-references: EMBL.X06370, NID:g31118; PIDN:CAA29668.1; PID:g31119
B, Halol. Chem. 266, 1746-1753, 1991
J. Biol. Chem. 266, 1746-1753, 1991
A, Title: Contributory effects of de Novo transcription and premature transcript the A, Title: Contributory effects of de Novo transcription and premature transcript the A, The Erect en unaber: A38672; MUD:91107677; PMID:1988448
A, Molecule type: DNA
A, Residues: 1-29 - (HAL>
A, Residues: 1-29 - (HAL>
A, Residues: 1-29 - (HAL>
A, Experimental source: carcinoma cell line A431-7
B, Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.
Nature 309, 806-8100, 1984
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number: A00641; MUID:84219729; PMID:6328312
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                                  ELEFAGCKKI FGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISAWPDSLP
                                                                     PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
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A; Molecule type: protein
A; Residues: 25-30,'8',32-51;454-467 < WEB>
F; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 2505-5208, 1985
A; Title: Identification of residues in the nucleotide binding site of the epidermal grow.
A; Reference number: A60143; MUID:85182650; PMID:2985580
                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Mesidues: 740-744, X', 746-747 < RUS>
R; Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
Nature 309, 270-273, 1984
A; Title: AFP-stimulated interaction between epidermal growth factor receptor and A; Reference number: A38023; MIID:8419154; PMID:6325948
A; Contents: annotation; receptor activity
                                                                                                                                                                                                                                                                                              A, Accession: A60143
                                                                                                                                                                                                                                  epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Homo-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999 C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; A33 R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.; Y
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Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression
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| A,Note:<br>R;Chen,<br>Cell 59,<br>A;Title: | A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell 59, 33-43, 1989 A;Title: Functional independence of the epidermal growth factor receptor from a domain r  | Db 602 ENNTL-VWKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGWVGALLLLL 658  Qy 664 VVVLGVVFGILIKRRQKIRKYTMRRLLQETELVBPLTPSGAMPNQAQMRILKETELRKV 723  |
|--|--|--|
| A;Refere<br>A;Conten<br>C;Commen           | 3; PMID:2790960<br>signal<br>r leads to internalization of the EGF-re  | Db 659 VVALGIGLFMRRHIVRKRTLRRLLQERELVEPLTPSGEAPNQALLRILKETEFKKI 715<br>Qy 724 KVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVS 783   |
| C,Geneti<br>A,Gene:                        | מט   | 716  |
| A; Map pc<br>C; Superf                     | A;COSE-Increment of State of S | Qy 784 RLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVH 843  |
| F;1-24/E<br>F;25-121                       | redicted <nat> predicted <nat></nat></nat>   | 770 KILGALCILS.VQLITQLGFFGCLIBDIVRERALMIGGGTTBLUNGVÇIANGGGTTBLUNG 03   |
| F;25-645<br>F;75-300<br>F;390-60           | 5-649/Domain: extracellular #status predicted <ext><br/>5-300/Domain: EGF receptor extracellular domain repeat <ee1><br/>90-600/Domain: EGF receptor extracellular domain repeat <ee2></ee2></ee1></ext>   | Db 836 RDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIYTHQS 895  |
| F;646-66<br>F;669-12<br>F;710-97           | pred:  | Qy 904 DVWSYGVTVWELMTFGAKFYDGIFAREIFDLLEKGERLPQFPICTIDVYMIMVKCWMIDS 963  |
| F;718-72<br>F;999-10                       | 718-726/Region: protein kinase ATP-binding motif   | 964 BCRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEE   |
| F;104/-1<br>F;128,17<br>F;745/AC           | .110/kegion: inhibitory<br>252,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic<br>stive site: Lys #status experimental  | Db 956 DSRPKFRELIIEFSKWARDPQRYLVIQGDERWHLFSPTDSNFYRALMDEEDMDDVVDADE 1015   |
| Query Ma<br>Best Loo<br>Matches            | / Match 45.4%; Score 3097; DB 1; Length 1210; Local Similarity 49.5%; Pred. No. 1.4e-119; Indels 108; Gaps 23;   | Qy 1023 YLVPQQGFPCPDPAPGAGGWVHHRHRSSTRSGGGDLTLGLBPSEEBAPRSPLAPSEGAG 1082<br>   |
| ò a  | 11 LLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 68   | Qy 1083 SDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSBDPTVPLPSETDGYVAPLTCSPQPEYV 1140  |
| <i>රු</i> සි                               | 69 ASLSFLQDIOBVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128  | Qy 1141 NQPDVRPQPFSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TP 1199  Db 1094 NQ-SVPKRPP.GSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTV 1142  |
| ` & £                                      | VTGASPGGLRELQLRSLTBILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR 18:   | Qy         1200 QGGAAPQPHPPPAFSPAFDNLYYWDQDPPERCAPPSTFKGTPTA 1243           D  |
| 8 &  |  | Oy 1244 ENPEYL 1249<br>           <br>Db 1193 ENAEYL 1198  |
| Ор   | 184 LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQOCSGRCRGKSPSDCCHNQCAAGCTGP 243   |  |
| & 8  | 248 KHSDCLACLHPNHSGICELHCPALVTYNTDTFESMPNPBGRYTFGASCVTACPYNYLSTD 307 :   | RESULT 5<br>A53183<br>epidermal growth factor receptor precursor - mouse   |
| ço<br>qa                                   | 308 VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQXIKANSKFIGITELE-FAG 366   | C:Species: Mus musculus (house mouse)<br>C:Date: O6-Jan-1995 #sequence_revision O6-Jan-1995 #text_change 18-Jun-1999<br>C:Accession: A53183; A43818; Z24942; A28941; S45325; I49543<br>R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.; |
| ે રે                                       | ٠.   | Genes Dev. 8, 399-413, 1994  A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor t A;Reference number: A53183; MUID:94170986; PMID:8125255  |
| 3 & i                                      | NLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLF 486   | A,Molecule type: mRNA<br>A,Molecule type: mRNA<br>A,Residues: 1-1210 <lue><br/>A,Cross-references: GB:U03425</lue>   |
| 8 8  | 422 NDELLKGKTKJHGQFSLAVVSENITSLGLKSLKEISDGDVIISGNKNLCYANTINWKKLF 481<br>487 RNDHOALLHTANRDEDECVGEGTACHOLCARGHCWGBGDTOCVNCSOFFBGGETVFECFV 546   | R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.<br>Oncogene 6, 673-676, 1991<br>b.Title. Commariann of BGB receptor semisones as a milds to study the ligand hinding sit   |
| 7 A  | GTSGQKTKIISNRGENSCKAIGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCKL 541   | •  |
| දු දු                                      | 547 LQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKP 606   | A,Molecule type: mkNA<br>A,Residues: 1-714 <avi><br/>A,Cros-references: GB:X59698<br/>R.Risinger D D . Serer: G</avi>  |
| ò  | DLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVGILL 663  | submitted to the EMBL Data Library, June 1992<br>A;Reference number: S24942<br>A;Accession: S24942   |

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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species Gallus gallus (chicken)
C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
E;Lax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennst: Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mol A;Reference number: A27720; MUID:88261272; PMID:3260329
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                  SVFONLOVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
                                                        ECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPS
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                                                                                                                                                             DOLFRNPHOALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE
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1191 TAENAEYLRVAPP 1203
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A. Residues: 699-64, X', 696-704, L', 706-707;989-992, XX', 995-996, X', 998-1000;1002-1009,
B. Hibbs, M. L.; Dunn, A. R.; Alexander, W. S.
Bubmitted to the EMBL Data Library, April 1994
A. Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor A. Perference number: S45325
A. Reference number: S45325
A. Status: preliminary
A. Rocession: S45325
A. Status: preliminary
A. Residues: 1-971, K', 973-1210 «VER.
A. Residues: 1-971, K', 973-1210 «VER.
A. Residues: 1-971, K', 973-1210 «VER.
A. Residues: B. C.; Das, S. K.; Andrews, G. K.; Dey, S. K.
Proc. Natl. Acad. Sci. U. S. A. 90, 55-59, 1993
A. Title: Expression of the epidermal growth factor receptor gene is regulated in mouse be a procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the process
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A;Residues: 12-20,22-132 <RES>
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
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Conservative 165; Mismatches 367; Indels 112;
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A;Residues: 969-971, 'K', 973-1115, 'D' <EIS>
A;Cross-references: EMBL:212608
R;Heisermann, G.J.; Gill, G.N.
Tible Chem. 263, 13152-13158, 1988
A;Tible: Epidermal growth factor receptor threonine and A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
A;Molecule type: protein
A;Residues: 689-694, 'X', 696-704, 'L', 706-707;989-992, 'XX', R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
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A;Status: translated from GB/EMBL/DDBJ
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Matches 629; Conserv
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G.W.; Foy, L.; No
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C;Species: 18mo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
C;Accession: A47253
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/p180erb84, a fourth member of the epidermal
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                                                                                                                                      CVKACPAGVIGENDTL-VWKYADANAVCOLCHPNCTRGCKGPGLEGCP---NGSKTPSIA
                                                                                                                                                                                                                                                                                                                                                                    LKETEFKKVIVVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956 MVKCWMIDADSRPKFRELIAEPSKWARDPPRYLVIQGDERMHLPSPTDSKFYRTLMEEED
                                                                                                     CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
                                                                                                                                                                                                                 656 SAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 PLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGNFLEESIDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
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A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
S.Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology <KIN>
F;724-732/Region: protein kinase ATP-binding motif
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A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nuclaic acid
A;Residues: 1-1308 <PLO>
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A;Accession: A27720
A;Molecule type: mRNA
A;Residues: 1-1223 (ALAZ)
A;Cross-references: GB:MZ0386
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M Cell 41, 719-726, 1985
A;Tille: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro A;Reference number: A00643; MUID:8528222; PMID:2988784
A;Accession: A00643; MUID:8528222; PMID:2988784
A;Accession: A00643
A;Residues: 585-123 anLb
A;Cross-references: GB:M10066
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.397-610/Domain: EGF receptor extracellular domain repeat <EE.2>
F.655-677/Domain: transmembrane #status predicted <TWM>
F.655-677/Domain: intracellular #status predicted <TWM>
F.678-1223/Domain: intracellular #status predicted <INT>
F.719-984/Domain: protein kinase ATP-binding motif
F.3127-315/Region: protein kinase ATP-binding motif
F.316-20.280, 315, 310, 342, 575, 580, 615, 315/Binding site: carbohydrate (Thr) (covalent) #status predicted
F.192, 650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F.687/Binding site: phosphate (Thr) (covalent) #status predicted
F.554/Active site: Lys #status predicted
F.1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
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;1-1223/Product: epidermal growth factor receptor #status predicted <MAT>
;31-654/Domain: extracellular #status predicted <EXT>
;81-307/Domain: EGF receptor extracellular domain repeat <EE1>
;397-610/Domain: EGF receptor extracellular domain repeat <EE2>
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| 9 WGLIAALIP FORAA  | Best        | imilarity 44.8%; Sect. 2.70-112; Lough 100;<br>Conservative 185; Mismatches 385; Indels 173; Gaps  | ପ୍ଧ                  | 1009 DEEDLEDMM                       |
| 10.000   | ò           | WGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY 6   | δ                    |                                      |
| 65 JPTWASLSELDOTOPHOCHYLANDOPHOLIALINGTHANDARDALATION 212  | qq          | :   :  | අු                   |                                      |
| 13   | Š           | LPTNASLSFLODIOEVOGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN   | ð                    |                                      |
| 128   WINDERSOCRATEGREGORGE PROPERTY OF THE PROPERTY IN 19   19   116    | QQ          | :           : ::   | <u>a</u>             |                                      |
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| 195   DINSESCREPESENCESENCESENCYCE/PREVISCREPTERCAGO 237   DB 21200   DS 11   | qa          |  | <u> </u>             |                                      |
| 179 SPHGSSCORCHRSCTYC-RCMCPTERRHCOTH/IRTHVCLOCARCYCPHYSD-CHRSCHAN 201   244 CTGRENDLACCHPRINGSIGLERICALACTATTTTESBRINGSTRYTSARCYCTARY 303   DP 1250   DP 1260   DP 1   | ò           | DINRSRACHPCSPMCKGSRCWGESSEDCQSLIRIVCAGGC-ARCKGPLPTDCCHEQCAAG   | Ši ti                |                                      |
| 244 CYDPHRIDOTALIPHRIGATCHEPALTYMYNDTPERANNEGRAPHYCACALAPORN 201  258 GSRCDTDCFACCHEPADGACATCCEOTOTALIPHRICALISE 353  364 BACKATEGALALIPHRIGATCHEPADTATALIPHRICALISE 363  365 U-VUSSSCOTALIPHRIGATCHEPADTATALIPHRICALISE 363  364 PACKATEGALALIPHRICATCHEPADTATALIPHRICALISE ACCOUNTING 365  365 THATALIANANILLIPHRICALISE TRANSFORTING AND AND AND AND AND AND AND AND AND AND  | qq          | STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG   | g ;                  |                                      |
| 238 G'SGLYON CONTROLLER OF THE | δ           | CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY   | è f                  |                                      |
| 104 LETDGGSCTLVCPLHNQEYTAEDCTRCGRCGAVCHAWGYCGLAMOYIGATEL 353 129 V-UDSSSCYRACPSSRAMEY-EBNOIRNCKECTDICPKACDGIGTGSLAMSAQTVDSSNIDK 355 154 FACCKITGGSLAELPESSPAGDPASNITARQYIGAMSKTIGTTELTXYLYIAAWDELPDLS 423 155 FINCTKINGALLFLYNGLIGGLGISMIGARSLRSLASGGALHHNYTHLCTWYTYAAWDELPDLS 415 156 FINCTKINGALLFLYNGLIGGLGISMIGARSLRSLASGGALHHNYTHLCTWYTYAAWDELPDLS 415 157 GARLANTGGRYLYSGLSLJILAKQGGTSLAGGARGHAWGRCPTACAVGGAPRACGECVEE 543 157 GARLANTGGRYLYSGLSLJILAKQGGTSLACHCWGRCPTOCVMCSOFLAGGRCVEE 543 158 GARLANTGGRYLYRSDRAKARCTREGWACHACGSSCAGFEDDCVACACHYCOPPERCORE 543 159 GALGGANSF-LAFTARRPEBECVGCAGPOORSIAELSANTYITDNSNICTYHTINWT 475 150 GALGGANSF-LAFTARRPEBECACOPCRINCTHSCVACACHYCOPPECVARCES 603 171 GARLACTAGGANST-VACOPTIAKAROOCHACACHACGSPACACHYCOPPECVACCSFRANTYITDNSNICTHINWT 475 150 GALGGANSF-LAFTARDARACTAGACHACHACACHACHACACHACACHACACHACACHA  | qq          | CSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNF   | 3                    |                                      |
| 298 V-VDSSĞCVRAĞPSSRARĞV-ERĞİRKİKÇETİLÇEKİCDĞİĞTGSLABAQIYDSSNIDK 355 364 PAGCKKITGSLAFLPESFDGDPASNITARQYIKANSKFIGITELIĞYLXISAWEDSLEDILS 423 365 PINCTKINOLI FUYDGUDENANITARQYIKANSKFIGITELIĞYLXISAWEDSLEDILS 425 416 PAGCKKITGSLAFLPESFDGDPASNITARQYIKANSKFIGITELIĞYLXIGAWEPANTDES 415 416 VERNILATIRATIRATELIĞYAĞILƏ AĞ | ò           | LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE   | RESULT               |                                      |
| 3-6 PACKTICKSLAFLPESFDGDPASNTAPQYICANSKTIGITELTCYLISAMPSPPDL 423 3-5 FINCTKINGALIPELYTGIHGDPYNAIEAIDPEKLAVFFTVREITGFALIGSMPPNATDES 415 3-5 FINCTKINGALIPELYTGIHGDPYNAIEAIDPEKLAVFFTVREITGFALIGSMPPNATDES 415 4-14 VPGNLQVIRGALIPELYTGIHGDPYNAIEAIDPEKLAVFFTVREITGFALIGSMPPNATDES 415 4-16 VPGNLQVIRGALIPTANRPEDECVGEGLACHGLGSKETSAGNLIHMYHLCFVHTVPWD 483 4-16 VPGNLQVIRGALIPTANRPEDECVGEGLACHGLGSKETSAGNLIHMYHLCFVHTVPWD 483 4-16 VPGNLQVIRGALIPTANRPEDECVGEGLACHGLGCOSKETSAGNLIHMYHLCFVHTYPWT 475 4-17 LFSTINGALVYBDRKAENTTAEGNACHGLGCOSKETSAGNLIHMYHLCFVHTYPWT 475 4-18 (1   1   1   1   1   1   1   1   1   1   | qq          | V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTVDSSNIDK   | proteir<br>N:Alte    | n-tyrosine kinas<br>rnate names: eni |
| 356 PINCTKINGALIPLYGIHGDPWAIREAIDPEKLAVEFTVEITIGENIGSWEPPWATDES 415 414 VPGNLQVIRGRILHNGAVELILGGOGISWIGHSTREIGSGLALIHNTHLCFVHTVPWD 483 415 VPGNLQVIRGRILHNGAVELILGGOGISWIGHSTREIGSGLALIHNTHLCFVHTVPWD 483 416 VPGNLQVIGGRILARAGGLACHGCARCHGAGGCAGGCCVBE 543 417 INTERPREPAGENCALACHGLACHGAGGCAGGCCVBE 543 418 GLESTINGALVIRDNRKAENCTARGAWCNHLCSSDCKAGGGPGPDGLSCRRFSRGRICIES 535 544 CRULGGLPREYWARHCLPCHPECQP-ONGSVTREGPEDACUSCRRFSRGRICIES 535 545 CNLVDGEFREFERGSICVECDPGCEAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCA   | ò           | FAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISAWPDSLPDLS   | C, Spec              | ies: Xiphophorus                     |
| 424 VPQNLQVIRGRILHNGAYSLTLQGLGISWIGLRSLRELGSGLALIHNYHLCFVHTVPWD 483  416 VPSNLQVIRGRILHNGAYSLTLQGCGISWIGLRSLRELGATITINSNLCYPHTINFT 475  417 VPSNLYTGGSVLYSGLSLILLLGGCGTSLTGGCGSERSISATITINSNLCYPHTINFT 475  418 QLFRNPHQALLHTANREDBECVGEGLACHQLCARGHCRGFOPQCTASGCEVEE 543  419 TIPSTINQRILHTANREDBECVGEGLACHQLCARGHCRGFOPQCTACGGFUSGCEVEE 543  410 TIPSTINQRILHTANREDBECVGEGLACHQCTACHGCGPDQCCACRRFSRGRICIES 535  411 CRVLQGLPREYNARHCLPCHPECQP -QNGSYTCFGFDBADQCAACHYDDPFCVARCPD 602  412 TIPSTINQRILHTANREDBECACQCPINCTTCHGCPBADCCACCHYRDPPFCVARCPD 603  413 TIPSTINQRILHTANREDBECACQCPINCTTCHGCPBADCCACCHYRDPFCVARCPD 605  414 TIPSTINQRILHTANREDBECACQCPINCTTCHGCPBADCCACCHYRDPFCCACRCPACCPD 603  415 TIPSTINGRILHTANREDBECACQCPINCTTCHGCPBADCTACCSHFKGGPRCYRRCPD 605  416 TIPSTINGRILHTANREDBECACQCPINCTTCHGCPBADCTACCSHFKGGPRCYRRCPD 605  417 TIPSTINGRILHTANREDBECACQCPINCTTCHGCPBADCTACCSHFKGGAMPRQA 710  418 TIPSTINGRILHTANREDBECACGCPTHTTCHGCACCHYRCPTRANGET 603  419 TIPSTINGRILHTANREDBECACGCPTHTTCHGCACCHYRCPTRANGET 603  410 TIPSTINGRILHTANREDBECACGARGTYRGINTDGGRANTRENGET 603  411 TIPSTINGRILHTANREDBEARNALGGARGTYRGINTHANGTOGACPTRANGET 603  411 TIPSTINGRILHTANREDLAGARYTWELMYCTGTARLAGGGRAPTKWA 808  411 TANNANGHPHHVRALGACCACSPTIQLYTQLMPHGCLLEYVBEHCONTGSQLLLMWCVQLA 808  412 TANNANGHPHHVRALGACCACSPTIQLYTQLMPHGCLLEYVBEHCONTGSQLLLMWCVQLA 808  413 TANNANGHPHHVRALGACCACCACTACTACTACTGCACCACTACTACTACTACTACTACTACTACTACTACTACT   | qq          | FINCTKINGNLIFLVTGIHGDPYNAIBAIDPEKLNVFRTVRBITGFLNIQSWPPNMTDFS   | C, Dace              | seion: S06142; 8                     |
| 416 VESNILVITIGGRAUINSGISLITIKOOGITESLOPESILEEISAGNIYITDNSNLLYYHTINWT 475  404 OLFRNHQALLHTANR PEDECVGEGLACHOLCARCHCWGPGPTOCVNCSQFLRGGCCVEE 543  476 TLESTINGRINEDRIKKABNCTAREANCTALCHCCARCHCWGPGPTOCVNCSQFLRGGCCVEE 515  514 CRULQGLEREYNAAHCLECHECOPOCKAWGPCRAFTCAHYCDPFCVARCPS 602  515 CNLYDGEFREENGSICVECPPOCKAWGPGPTSHOCTYCGHRYGPROPWCKCPD 595  603 GVRDLSYMDIWKFPDERGACOPCPINCTHSCVDLDDXCCPAGGRASPL 651  51 CNLYDGEFREENGSICVECPPOCKAWGDGLITCHGPGPDNCTKCSHPKOGPNCWKCPD 595  603 GVRDLSYMDIWKFPDERGACOPCPINCTHSCVDLDDXCC   | ò           | VPQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRSLGSGLALIHHNTHLCFVHTVPWD   | Nature<br>Nature     | 341, 415-421,<br>Novel mitativ       |
| 484 QLFRNPHOALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE 543   | Ор          | VFSNLVTIGGRVLYSGLSLLILKQQGITSLQFQSLKEISAGNIYITDNSNLCYYHTINWT   | A; Refer             | rence number: S(                     |
| 476 TLFSTINRINGLED THE THIN THIN THIS THIN THIS THIN THIS THIN THIN THIN THIN THIN THIN THIN THIN  | ò           | QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE   | A; Accer<br>A; Molec | selon: SU6142<br>cule type: DNA      |
| 544 CRVLQGLPREYVNARHCLPCHPECQP-ONGSVTCFGPEADQCVACAHYKDPPFCVARCB 602  | qq          | TLFSTINQRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIES   | A; Cross             | a-references: El                     |
| 536 CNLYDGEFREENGSICYGCDPOCEKNEDGLICTCHORDPINCTK(SHFKOGPNIVEKUPD 595 603 GVKPDLSYMPINKEPDEGACOPCINCTHSCVDLDDKGCPAEGRASPL 651   :=   :=   :=  | ò           | CRVLQGLPREYVNARHCLPCQP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPS   | Oncoger              | ne 6, 73-80, 195                     |
| 603 GVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEGRASPL 651  | qq          | CNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGFGFDNCTKCSHFKDGPNCVEKCPD   | A; Refe              | rence number: S1                     |
| 1:   | ò           | GVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPL  | A; Acces             | ssion: Si3809<br>is: preliminary     |
|  | qq          | ::  :  :   | A;Molec<br>A;Resic   | cule type: DNA<br>dues: 821-1025,    |
|  | ò           | TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQA   | A; Cross<br>C; Genet | s-references: El<br>:ics:            |
| 111 QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE 770   | QΩ          | IAAGVIGGLFILVIVGLTFAVYVRRKSIK-KKRALRRFL-ETELVEPLTPSGTAPNQA   | A, Gene              | : mrk<br>oosition: Y                 |
|  | è           | OMBILKETERERVKVI GSGA EGTVVKGIWI POGENVKI PVA I KVI BENTSEKANKEII DE   | A; Intro             | ons: 872/3; 898,                     |
| 71 AYYMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLNWCNQIA 830 769 ALIMASMPHPHLYRLLGVCLSPTIGLYTQLMPHGCLLEYYHEHKDNIGSQLLLNWCVQIA 828 831 KGMSYLEDVRLVHRDLAARNVLVKSPNHYKITDFGLARLLDDTETEYHADGGKVPIKMMA 890  | 7 A         |  | C; Keywo             | ords: ATP; growl                     |
| 769 ALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIA 828  831 KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA 890  829 KGMMYLERRLTHQEDVARVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKWPIKMMA 898  891 LESILRRRFTHQEDVWSYGYTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 950  892 LESILRRRFTHQSDVWSYGYTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 950  893 LECIHYRKTHQSDVWSYGYTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID 948  951 VYMINVKCWMIDSECRPRFELVSEFSRMARDPQRFVVIQNED-LGPASFLDSTFYRSLL 1009  954 VYMVWKCWMIDADSRPKFKELVSEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLL 1008  | è           | AVIMACUCEDUVEDI I CT CT TETRIOI UTOT UTOT I DUVERIDED COODI I MILIONOTA  | F;26-13              | 166/Product: kin                     |
| 1  | 3 6         | ALTERNACIONE L'ACCEPTATION CONTRACTOR DE L'ACCEPTATION DE | F;715-7              | 723/Region: pro                      |
| ### ### ### ### ######################   | 3 8         | ALLINASHIDRIKALIVALDIN KULGAVULDSY I I QUA I QURRYAGULDE I VREHADIN GOQULDINAV VQIA<br>KOMOVI EDIDDI MUDDI AABAMA MKOBAHAWI HIDRIYA ABI I DI DERBOUADOKKADI KAAA   | Query                | Watch                                |
| SOURCE   S   | ;<br>;<br>; | ACTION TO THE CONTROLLAR OF THE CONTROLL OF CONTROLL OF THE CO | Match                | nocai Simitafily<br>nes 568; Conser  |
|  | } }         | LESILERE THOSDWAY GYTWELMTEGA KPYDGIPABEI PDIJEKGERI POPPICTID   | λΌ                   | 4 AALCRWGLL                          |
| 951 VYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVUIQNED-LGPASPLDSTFYRSLL 1009         Qy         60 L           '  | g 20        |  | qq                   | 8 AALLQLI                            |
|  | Š           | VYMIMVKCMMIDSECREBERIVSERSRAARDEOBEVVIONED-I.CBASEIDSTEVESII.  | δ                    | = [                                  |
| 1010 EDDDMGDLVDAEEXI.VPOOGFFCPDPAPGAGGMVHHRHBSSSTREGGGDLTLGLEPSERE 1069  | ; a         | VANVACANI DADSREKKELAAERSAARREDENYI.   | đ                    | -띰                                   |
|  | l è         |  | λ̈́O                 | 120 GDPLNNTTP                        |

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se (EC 2.7.1.112) mrk-Y precursor - southern platyfish idermal growth factor receptor homolog; kinase-related transforming maculatus (southern platyfish) sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 S13809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nal activation of the melanoma inducing Xmrk oncogene in Xiphophor
13807; MUID:91125882; PMID:1846957
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mal growth factor receptor; protein kinase homology
th factor receptor; phosphotransferase; transmembrane protein; tyre
sequence #status predicted <SIG>
nase-related transforming protein (Tu) #status predicted <WAT>
tein kinase homology <KIN>
tein kinase ATP-binding motif
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| | | ::|| ;:|| ;: | | :: | | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.7%; Score 2636; DB 1; Length 1166;
;y 44.7%; Pred. No. 9.2e-101;
prvative 169; Mismatches 388; Indels 146; Gaps
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MBL:X16891, NID:g65290, PIDN:CAA34770.1, PID:g65291
W.; Schartl, M.
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HBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
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YKQNGRIRPIVAENPEYL 1285
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| 쉽       | 123 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP 179     | •                                      |
|---------|--|--|
| ò       | 180 ALTLIDINRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238   | VY 1240 TE                             |
| qa      | :  | Db 1146 LE                             |
| λο<br>· | 239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298   | RESULT 9                               |
| qq      | 240 HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPRIYDIVSHQVVDNPNIKYTFGAACVKE 299    | A36223<br>kinase-related t             |
| ò       | 299 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358   | C;Species: Homo<br>C;Date: 04-Oct-1    |
| qa      | 300 CPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVCDGIGIGSL-SNTIAVN 356   | C; Accession: A36<br>R; Kraus, M.H.; J |
| λo      | 359 ITEL-EFAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISA 414      | A;Title: Isolati                       |
| q       | SDPHYKIGTMDPEHLWNLTTVKE  | A; Accession: A36                      |
| ò       | PDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRE                             | A; Molecule type:                      |
| QQ      | 414 WPENWISLSVFQNLEIIRGRITFSRGFSFVVVQVRHLQWLGLRSLKEVSAGNVILKNTLQ 473   | A; Kesiddes: 1-13<br>A; Cross-referenc |
| ò       | 474 LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ 533   | Proc. Natl. Acac                       |
| QQ      | NECSEDGCW-PGPIMCV  | A;Reference numb                       |
| ò       | JGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACH                              | A; Accession: 15:<br>A; Status: prelir |
| qq      | 526 VDRGGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCSKSAHFQDG 585   | A; Molecule type:<br>A; Residues: 1-55 |
| ò       | 594 PFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTS 653   | A;Cross-reterenc<br>C;Genetics:        |
| q       | 586 PQCIPRCPHGLGDGDTL-IWKYADKWGQCQPCHQNCTQGGSGPGLSGCRGD-IVSHSSL 643    | A;Gene: GDB:ERBE<br>A;Cross-referenc   |
| ò       | 654 IVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNOAQMR 713   | A, Map position:<br>C, Superfamily: u  |
| οp      | 644 AVGLVSGLITVIVALLIVVLERRRRIK-RKRTIRCLLQEKBLVEPLTPSGQAPNQAFLR 702    | C; Keywords: ATP,<br>F;707-972/Domair  |
| ò       | 714 ILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYV 773   | F;715-723/Region                       |
| 업       | 703 ILKETEFKKDRVLGSGAFGTVYKGLWNPDGENIRIPVAIKVLREATSPKVNQEVLDEAYV 762   | Query Match<br>Best Local Sin          |
| ò       | 774 MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM 833   | Marches 524                            |
| d       | 763 MASVDHPHVCRLLGICLTSAVQLVTQLMPYGCLLDYVRQHQERICGQWLLNWCVQIAKGM 822   | 2 ;                                    |
| ò       | 834 SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES 893   | 11                                     |
| Д       |  | Oy 68 NZ                               |
| ò       | 894 ILERRETHOSDVWSYGVTVWELMTEGAKPYDGIPARFIPDILERGERLPOPPICTIDVYM 953   | Db 71 N7                               |
| : A     | ::   | Qy 128 PV                              |
| ò       | 954 IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD 1013  | Db 126                                 |
| DP      | ::   | 188                                    |
| ò       | 1014 MGDLVDABEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS 1073 | 179                                    |
| q       | :   :   :  :  <br>1000DVVDADEYLLPYKRI                                  | Oy 247 PF                              |
| ò       | 1074 PLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHDPSPLORYSEDPTV-PLPSETDGYVAPLT 1132 | Db 238 ÞÇ                              |
| 셤       | 105  | Oy 307 D                               |
| ò       | PGKNG 117  | Db 297 bg                              |
| qq      | RLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTNQNS 111                        |  |
| ò       | 1180 VVKDVFAFGGAVENPEYLTPQGGAAPOPHPPPAFSPAFDNLYYWDODPPERGAPPSTFKG 1239 | Db 351 F                               |
| Ob      |  | Qy 424 VE                              |
|         |  |  |

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ad transforming protein (erbB3) (EC 2.7.1.-) precursor - human ti-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 A36223; IS9164 W.; Miki, T.; Popescu, N.C.; Aaronson, S.A. cad. Sci. U.S.A. 86, 9193-9197, 1989 ation and characterization of ERBB3, a third member of the ERBB/epidermal amber: A36223; MUID:90083224; PMID:2687875
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ular cloning and expression of another epidermal growth factor receptor-r mber: IS9164; MUID:90311312; PMID:2164210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nces: GDB:119880; OMIM:190151
: 12q13-12q13
unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
P; phosphotransferase
in: protein kinase homology «KIN»
on: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.7%; Score 2366.5; DB 2; Length 1342;
imilarity 39.9%; Pred. No. 1.1e-89;
; Conservative 197; Mismatches 458; Indels 135; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559,'G',561-957,'F',959-1063,'G',1065-1342 <RES>
nces: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
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e: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                          liminary
pe: mRNA
-1342 <KRA>
ences: GB:M29366
PTAENPEYLS 1250
                                            PAAENLEYLG 1156
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DB 2; Length 1339

33.5%; Score 2280.5;

seq4-369-383-12.rpr

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A;Cross-references: GB:U29339; NID:g915389; PID:g915390
A;Bxperimental source: liver
A,Bxperimental source: liver
A,Bxperimental source: liver
C;Coment: The authors translated the codon AAC for residue 369 as Thr and GTT for residue C;Coment: This protein is a functional heregulin receptor that transduces signals to ti C;Genetics:
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NyAlternate names: ErbB3 protein, HER3 protein
C;ppecies: Rattus norvegicus (Norway rat)
C;pacession: JC4387
C;Accession: JC4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombina A;Reference number: JC4387; MUD:96096535; PMID:8522190
A;Accession: JC4387
A;Residues: 1-1339 cHEL>
                                                                                                                                                      THCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                                                                                                                                                     591 HGVLG--AKGPIXKYPDVQNECRPCHENCTOGCKGPELQDCLGQTLVLIGKTHLTMALTV
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                                                                                                                              EECRVI.QGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                                                                                                                             SGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSA
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                                               DQLFRNPHQALLHTA - NRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                                                    TKVLRGPTEERLDIKHNRPRRDCVAEGKVCDFLCSSGGCWGPGPGOCLSCRNYSRGGVCV
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LEIVLTGHNADLSFLQWIREVTAYVLVAMNEFSVLPLPNLRVVRGTQVYDGKFAIFVM--
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                                                                         LAALCRWGLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
                                                                                                                LOVLC----FLLSLARGSEMGNSQAVCPGTLNGLSVTGDADNQYQTLYKLYEKCEVVMGN
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Best Local Similarity 40.1%; Pred. No. 3.6e-86;
Matches 515; Conservative 173; Mismatches 438;
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| Db 117 GLEGCPNGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 172       | Qy 697 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLR 756 | Qy 757 ENTSPKANKEILDEAVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR 816  | Qy 817 IGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE 876  | Qy 877 YHADGGKVPIKWMALESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLE 936    :               | Qy 937 KGERLPQPPICTIDVYMIMVKCMMIDSECRPRERVSEFSRMARDPQRFVVIQ-NEDLG 995 | Qy 996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHSSSTRSG 1055 | Qy 1056 GGDLTLGLEPSEEBAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110 | QY         1111 RYSEDPTVPLPSET DGYVAPLTCSPQPEXVNQPDVRPQPPSPREGPLPAARPAGATLE 1168 | Qy         1169 RAKTLSPGKNGVVKDVF  | ü      | A; Itle: The erbB gene of avian erythroblastosis virus is a member of the src gene family Reference number: A00644; MUID:84026539; PMID:6313229 A; Reference number: A00644 A; Molecule type: DNA A; Residues: 1-604 < YAMA A; Residues: 1-604 < YAMA A; Cross-references: GB:K01216; NID:9209676; PIDN:AAA42400.1; PID:9209678 B; Debbire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, Science 224, 1456-1459, 1984 A; Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of A; Reference number: A38022; MUID:84223957; PMID:6328658 | A,Molecule type: DNA A;Rolecule type: DNA A;Rosidues: 1-28,'W',30-139,'F',141-145,'V',147-152 <deb> A;Rossidues: 1-28,'W',30-0006 C;Genetics: C;Genetics: A;Gene: exbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: procedene; phosphotransferase; transforming protein; tyrosine-specific F;130-395/Domain: protein kinase homology <kin> F;130-395/Domain: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted</kin></deb> |
|--|---|---|--|--|---|---|--|--|--|--------|---|---|
| Db '759, LAVGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVKQHRETLGPQLLLANWGVQIAK 818 | QY 832 GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMAL 891 | Qy 892 ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV 951 | QY 952 YMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFYRSLLED 1011 | QY         1012 DDMGDLVDAËEYLVPQQFFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE 1068           I | QY 1069EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT 1103<br>                   | QY 1104 HDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQP 1143                   | OY 1144 DVRPOPPSPREGPLPAARPAGATLERAKTLSP-GKNGVVKDVF 1185             | Oy 1186 AFGGAVENPEYLTPQGGAAPQPHPP 1210  Db 1192EEYEYMNRKRRGSP-PRPP 1209          | TVEVUT 11 TVFVLT | nd pro | C;Genetics: A;Gene gag-env-erbB C;Genetics: A;Gene: gag-env-erbB C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Reywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p F;1-6/Product: gag protein (fragment) #status predicted <gng> F;7-59/Product: protein (fragment) #status predicted <env> F;60-698/Product: protein tyrosine kinase erbB #status predicted <erb> F;202-210/Region: protein kinase ATP-hinding motif F;229/Active site: Lys #status predicted</erb></env></gng>  | · · · · · · · · · · · · · · · · · · ·   |

Length

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Query Match
Best Local Similarity
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Matches 345;
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;135-400/Domain: protein kinase ATP-binding motif
F;143-151/Region: protein kinase ATP-binding motif
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                                                                                                         587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                          647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                             NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                                                                        MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                                                                                                                                                                                    APNQAHLRILKETEFKKVKVLGSGAFGTIYKGLMIPEGEKVKIPVAIKELREATSPKANK
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                                                       Gaps
                                                       126;
  Length 604;
                                                    Indels
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76; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VONOIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-
25.0%; Score 1703; DB 1; 52.2%; Pred. No. 6.6e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
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R;Vennstroem, B:
Bubmitted to the EMBL Data Library, March 1993
A;Reference number: 835743
A;Accession: 838745
A;Molecule type: DNA
A;Cross-references: EMBL:X12707
C;Genetics:
A;Gene: exbB
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                                                    Conservative
                           Similarity
                        Best Local Sim:
Matches 360;
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C;Species: avian erythroblastosis virus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                996 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLG 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VEPLTPSGEAPNOAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 GPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                                            LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
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Score 1640; DB 2;
Pred. No. 2.3e-60;
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C.Keywords: ATP; phosphotransferase
F;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
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54.9%;
                                                                                                                  Conservative
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1065 PSEEEAPRSFL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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                                                                                                                                                                                                                                                 118 APNQAHLRIIKETEFKKVKVLGFGAFGTVYKCLWIPEGEKVTIPVAIKELREATSPKANK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 CVQIAKGMNY1EERHMVHRDLAARNVLVKTPQHVKITDFGLAKQLGADEKEYHAEGGKVP 297
                                                                                                                                        59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                                                                                                    178 EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP
             CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                    EILDEAYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   946 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 ICTIDVYMIMVKCWMSGADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHLPSPTDSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 -PVREDGFL------PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISKLPMDSRXQN
                                                                                                                RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                   MPNQAQMRII.KETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                             3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | | : | | : | | STITIMEEEDWEDIVDADEYLVPHOGFF------NSPST
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|     | Description                   | Human heregulin 2 | Human tyrosine kin | HER2 transgene pla | Human HER2 (ErbB2) | HER-2/neu protein. | Human HER-2/neu on | Human HER-2/neu pr | Amino acid sequenc | Human HER-2/neu pr | HER2/neu amino aci |
|-----|-------------------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|     | ID                            | AAY92620          | AAE12130           | AAB60167           | AAU74545           | AAW01111           | AAW92406           | AAB21198           | AAY84780           | AAB85458           | AAG88267           |
|     | DB                            | 21                | 22                 | 22                 | 23                 | 17                 | 20                 | 21                 | 21                 | 22                 | 22                 |
|     | Query<br>re Match Length DB I | 1255              | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               | 1255               |
| æ ( | Query                         | 98.8              | 98.8               | 98.8               | 98.8               | 98.7               | 98.7               | 98.7               | 98.7               | 98.7               | 98.7               |
|     | Score                         | 6720              | 6720               | 6720               | 6720               | 6714               | 6714               | 6714               | 6714               | 6714               | 6714               |
| ;   | Result<br>No.                 | -                 | 7                  | m                  | 4                  | S.                 | 9                  | 7                  | æ                  | თ                  | 10                 |

| Human Her-2 protei Human Her-2/neu pr Human Her-2/neu po Human Her-2/neu po Sequence of c-erbB Human hER-2/neu po Rat Her-2/neu pr Rat Her-2/neu prot Rat Her-2/neu prot Amino acid sequenc Mouse Her-2/neu ex Her-2/neu extracel Mouse Her-2/neu ex Human HER-2/neu ex Human HER-2/neu ex Human HER-2/neu ex Human HER-2/neu ex Human HER-2/neu fu Her-2/neu extracel Her2-GM-CSF immuno Extracellular HER- Human ErbB2 oncopr Human ErbB2 cocopr Human ErbB2 extrac DCBscFv-erbB2EC fu Extracellular port Amino acid sequenc Human ErbB2 extrac DCBscFv-erbB2EC fu Extracellular port Amino acid sequenc Human ErbB2 extrac DCBscFv-erbB2EC fu Extracellular port Amino acid sequenc Human ErbB2 extrac DCBscFv-erbB2EC fu Extracellular port Amino acid sequenc  | prote prote prote prote prote prote prote epide                  |
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Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope. /label= insertion region
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59.73
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dalum I;
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/label= insertion region
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Birk P, Karlsson G;
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins). e.g. human prostate specific membrane antigen (PESM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8B). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 First T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8B comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8B and Her2, respectively.
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                                                                      The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HBR-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of confirm transduction of polynucleotides into hosts and so primers for the detection of confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HBR-2. Compounds of the invention are designed based on the HBR-2 antigenic peptide
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                     The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and pl85au). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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16-MAR-2000; 2000US-0189844.
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is characterised by the overexpression of an epidermal growth factor receptor (BrbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladdar, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating enviral, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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   LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                                                                    HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                        IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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676..1255
//label= Intracellular domain
/noce="claimed domain, useful for immunisation"
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Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ax vivo with a viral vector that directs expression of the polypeptide.
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LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
        LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILRRRFT
                                           901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                  IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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for treating or
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/note= "region which elicits immune
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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for vaccinating against breast, ovarian, colon, lung and
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                                                       IDSECRPRERIVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
 HQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYM1MVKCWM
                                                                                                                EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                              AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                            1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                        NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
                                                                                                                                      NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents of e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                   EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                                                   GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                                                                              an erbB 2 receptor protein designated SPLICE the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                  SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder; wound healing.
                                                                                                                                                                                                                                                                                                               Amino acid sequence of the SPLICE erbB-2 receptor protein.
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erbB-2, inhibitors of
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                                                                                          1200
                                                                                                        The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostet cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigen-presenting cells, useful as vaccines for eliciting o enhancing an immune response to HER-2/neu protein, particularly for treating or preventing cancer, e.g. breast cancer
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Matches 1240; Conser
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The present invention describes isolated prepared HER2/neu epitopes (I).

Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

Culture in vitro and binds to a complex of an epitope (I), bound to a

chuman leukocyte antigen (HLA) molecule; (2) a peptide (I) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

cc acids that have 100% identity with a native peptide sequence of HERZ/neu;

(C) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II) and a pharmaceutical

excipient; (4) an isolated nucleic acid encoding (II). (I) has cytostatic

and immunostimulant activities, and can be used in vaccines. (I), (II)

and (III) are useful for inducing callular immune responses for the

prevention and treatment of cancer. (I) and (II) are useful for

monitoring or evaluating an immune response to a tumour-associated

antigen when incubated with a T lymphocyte to (I) or (II). Epitope

based vaccines mean that immunosuppressive epitopes may be combined to

confident antigens may be avoided. Selected epitopes may be combined to

enhance immunogenicity. The possible pathological side effects caused by

Infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune response to multiple

convolutes provides the opportunity to combine epitope-based anti-tumour

cumultiple tumour-associated molecules addressing the problem of tumour-

tumour variability and reducing the likelihood of tumour example in a reducing the likelihood of tumour example in a reducing the likelihood of tumour example in a reducing the likelihood of sequences used in
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
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cancer -
                                                                                                                                                                                                                                                                                                                                              Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                       GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                             AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                                          1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
                                                          Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
                                         GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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                                                                                                                                    AAE20479 standard; Protein; 1255 AA
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                   AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                   1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                  GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                            Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain
                                                                                                                                                                                                                                                                                        Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                                                  Human Her-2/neu oncogene-encoded p185 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "phosphorylation domain'
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/note= "extracellular domain"
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SMITHKLINE BEECHAM BIOLOGICALS.
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protein the fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of a animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated concer, especially breast, ovarian, colon, lung or prostete cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
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                                                                                                                                                                                                                                                                                               order to inhibit the development of cancer in a patient.
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Z/neu or a polynucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLI
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                 IDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                             EEYLVPQQGFFCPDPAPGAGGWVHIRHRSSSTRSGGGDLTLGLEPSEEBAPRSPLAPSEG
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AAR39568 ID AAR3

RESULT

Houston

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Qy 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Db 1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140

Qy 1141 NQPDVRPQPPSPRGGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Db 1141 NQPDVRPQPPSPRGGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200

Qy 1201 GGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPSTFKGTPTAENPEYLGLDVPV 1255

Db 1201 GGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255

Search completed: July 22, 2003, 08:41:01

Sob time: 43:9774 sec8
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 101002:\*

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## SUMMARIES

|   |        | Description     |      |        |      |      |      | ٠      |      |      | AAB85458 Human HER-2/neu pr |        |
|---|--------|-----------------|------|--------|------|------|------|--------|------|------|-----------------------------|--------|
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|   |        | Lengt!          | 125  | 125    | 125  | 125  | 125  | 125    | 125  | 125  | 1255                        | 125    |
| æ | Query  | Match Length DB | 98.9 | 98.9   | 98.9 | 98.9 | 98.8 | 98.8   | 98.8 | 98.8 | 98.8                        | 98.8   |
|   |        | Score           | 6735 | 6735   | 6735 | 6735 | 6729 | 6729   | 6729 | 6729 | 6729                        | 6729   |
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| 25 23 AAE24067<br>25 23 AAM51143<br>25 23 AAM51143<br>25 23 AAM51143<br>25 23 AAM51199<br>26 21 AAB21199<br>27 AAB21199<br>28 23 AAM511199<br>29 23 AAM511199<br>20 23 AAM51151<br>20 23 AAM51151<br>20 23 AAM51152<br>21 AAB21200<br>22 AAM51152<br>23 AAM51153<br>24 AAM51153<br>25 23 AAM51153<br>26 23 AAM51149<br>27 23 AAM51149<br>28 23 AAM51149<br>29 23 AAM51149<br>20 23 AAM51145<br>21 AAB51200<br>22 AAB61593<br>24 11 AAR06222<br>23 AAM51168<br>24 11 AAR06222<br>24 AAB68420<br>25 AAB68420<br>26 23 AAE68420<br>27 AAE68420<br>28 23 AAE68420<br>29 23 AAE68420<br>20 23 AAE68420<br>20 23 AAE68420<br>21 AAE68420<br>22 AAE68420<br>23 AAE68420<br>24 AAE68420<br>24 AAE68420<br>25 AAE68420<br>26 23 AAE68420<br>27 AAE68420<br>28 AAE68420<br>29 AAE68420<br>20 23 AAE68420<br>20 23 AAE68420<br>20 23 AAE68420<br>21 AAE68420<br>22 AAE68420<br>23 AAE68420<br>24 AAE68420<br>26 27 AAE68420<br>27 AAE68420<br>28 AAE68420<br>29 AAE68420<br>20 23 AAE68420 | 1255<br>1255<br>1255<br>1255<br>1255<br>1255<br>1256<br>1256   |         | Her-2/neu | Human Her-2/neu on<br>Human Her-2/neu on | TO SOL | east | HER-2/n | Rat HER-2/neu prot | Rat Her-2/neu onco | Mouse Her-2/neu pr | Amino acid sequenc | Mouse Her-2/neu on | Human HER-2/neu fu | Her-2/neu extracel | Mouse Her-2/neu ex | Mouse Her-2/neu ex | Human HER-2/neu fu | Her-2/neu extracel | Her2-GM-CSF immuno | Extracellular HER- | Human Her-2/neu on | Human ErbB2 oncopr | Human ErbB2 extrac | DC8scFv-erbB2EC fu | Extracellular port | Amino acid sequenc |      | Human Her-1 protei | epide | Amino acid sequenc | Human protein for |    |         | Human protein for | Human epidermal gr |
|---|--|---------|-----------|--|--------|------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------|--------------------|-------|--------------------|-------------------|----|---------|-------------------|--------------------|
|   | 1255<br>1255<br>1255<br>1255<br>1256<br>1256<br>1256<br>1256   | AAE2406 | AAE204 /  | AAMSI14                                  |        |      |         | AAB2119            | AAM5114            |                    |                    |                    |                    | AAM5114            |                    |                    | AAB2120            | AAM5114            |                    |                    |                    |                    |                    |                    |                    |                    |      | ·                  | ·     |                    |                   |    | AAE2048 | AAE2048           | ABP5176            |
|   |  |         |           |  |        |      |         |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | _                  | _    | _                  | _     | _                  | _                 | 7  | 6       | 0                 | 0                  |
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### ALIGNMENTS

|   |                    |                           | e immunity;  |          |                     |   |        | insertion"  | epitope insertion"   | ingertion"  | =                                 | TIDE CTON                   |
|---|--------------------|---------------------------|--|----------|---------------------|---|--------|---|--|---|---|-----------------------------|
|   |                    |                           | Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope. |          |                     |   |        | epitope   | epitope  | , and the same  | oni tono  | 34001400                    |
| T 1<br>620<br>AAY92620 standard; Protein; 1255 AA.<br>AAY92620; | :000 (first entry) | Human heregulin 2 (Her2). |  | sapiens. | Location/Qualifiers | /label= N-terminal<br>/note= "mature polypeptide" | 525    | /label= insertion region<br>/note= "suitable For foreign epitope insertion" | 5973<br>/label= insertion region<br>/note= "suitable For foreign | 103117<br>/label= insertion region<br>/note= "anitable For foreign enitone insertion" | 149-163<br>  Jabel = insertion region<br>  Ante = "enitable For foreinn | /more- surcapie for foreign |
| RESULT 1 AAY92620 ID AAY92620 XX AC AAY92620;                   | 10-AUG-2000        | Human h                   | Heregul<br>self-pro  | Ното ва  | Key                 |   | Region |   | Region   | Region  | Region  | Domain                      |
| RESU<br>AAY9<br>ID<br>XX<br>AC                                  | 占 <b>2</b>         | X E X                     | <u> </u>   | *8       | # E                 | FT  | FI     | FF  | HH   | FFF   | . F. F. F.  | FT                          |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the human heregulin 2 (Her2) sequence. Immunogenic analogues Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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/note= "suitable for foreign epitope insertion"
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytcoxic T-lymphocyte) group derived from the PA and/or at least 1 if itst T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/mrine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.

# Sequence 1255 AA;

ö 240 540 120 180 180 240 300 300 360 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360 420 420 480 480 9 9 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA ELTYLPTNASLSFLODIQEVQQYIKANSKFIGITELQRLRIVRGTQLFEDNYALAVLDNG YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL Gaps ö Length 1255; Indels Score 6735; DB 21; Pred. No. 0; 2; Mismatches 11; 5; 98.98; Matches 1242; Conservative Similarity 61 121 121 181 181 241 241 301 301 361 421 421 481 Query Match Best Local 9

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/note= "Antigenic epitope"
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                                                                              peptides) with enhanced bigings to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCB), to confirm transduction of polynucleotides into host cells (APCB), to confirm transduction of polynucleotides into host cells (APCB), to confirm transduction are designed based on the HER-2 antigenic peptide
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                  The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HBI and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers
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is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating enuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastcocelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                                          IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
           LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                    HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                        IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-mayransinoid conjugate; cancer; tumour; breast; estomach; endometrium; salivary gland; lung; kidney; colon; colorect; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; gland disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; astromal disorder; inflammatory disorder; angiogenic disorder; inflammatory disorder;
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           Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The product of early spressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                                                            Length 1255;
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/label= Intracellular domain
/note= "claimed domain, useful for immunisation"
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EEYLVPQQGFFCPDPAPGAGGWHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                   IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                          AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                   NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                               EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
                          HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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93US-0033644.
93US-0106112.
95US-0414417.
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              HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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Matches 1240; Conservative
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Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

Culture in vitro and binds to a complex of an epitope (I), bound to a

culture antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

cotids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (III) comprising (II) and a pharmaccutical

excipient; (4) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic

and immunostimulant activities, and can be used in vaccines. (I), (II)

and (III) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (I) and (II) are useful for

and (III) are useful for inducing cellular sample form a patient and

cecting the presence of bound T lymphocyte sample form a patient and

detecting the presence of bound T lymphocyte set (I) or (II). Epitope

conditions mean that immunosuppressive epitopes may be present

in whole antigens may be avoided. Selected epitopes may be present

in whole antigens may be avoided. Selected epitopes may be combined to

cenhance immunogenicity. The possible pathological side effects caused by

infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune response to multiple

celected antigens from the same pathogen. Epitope-based anti-tumour

vaccines provides the opportunity to combine epitopes derived from

while, ble tumour-associated molecules addressing the problem of tumour-

tumour variability and reducing the likelihood of tumour escape due

cut exemplification of the present invention.
 1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                                   Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated prepared {\tt HER2/neu} epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer-
                               GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                          NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
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N-PSDB; AAD38904.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, preventions, eag., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to call the invention is useful for stimulating a T cell response in a human patient, as probe or primer for nucleic acid hybridisation, to call the centively form duplax molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full complementary and to direct expression of a polypeptide in appropriate host cells. The composition is useful in gene therapy. The reasons of the inmunotherapy of breast cancer and other Her-2/Neu-
                                                                                                                                                                                                                     Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                         /note= "Naturally processed HLA-B44-restricted epitope"
          NOPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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prevention and diagnosis of cancer, preferably breast cancer
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                                                                                                                                                            Human Her-2/neu protein.
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Mcneill PD, Vedvick TS;
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                                                                                                     1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1140
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                                   1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEVV
                                                                             The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular Gomain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines
                                                                 NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                        GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                                                                                                                                                                                                                             Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                                       Human Her-2/neu oncogene-encoded p185 glycoprotein.
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of phosphorylation domain (or its DeltaPD fragment). An immune administering the fusion protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells concing the fusion protein, and delivering the transfected cells concerned animal. The fusion protein, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
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The invention relates to a method for innibiting ueverophwent of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polymucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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                                                                                                                                                                                                                                                                                       YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                               YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGMSYLEDVR
                                                                                                       LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; M
Hodgkin's lymphoma; T cell therapy.
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